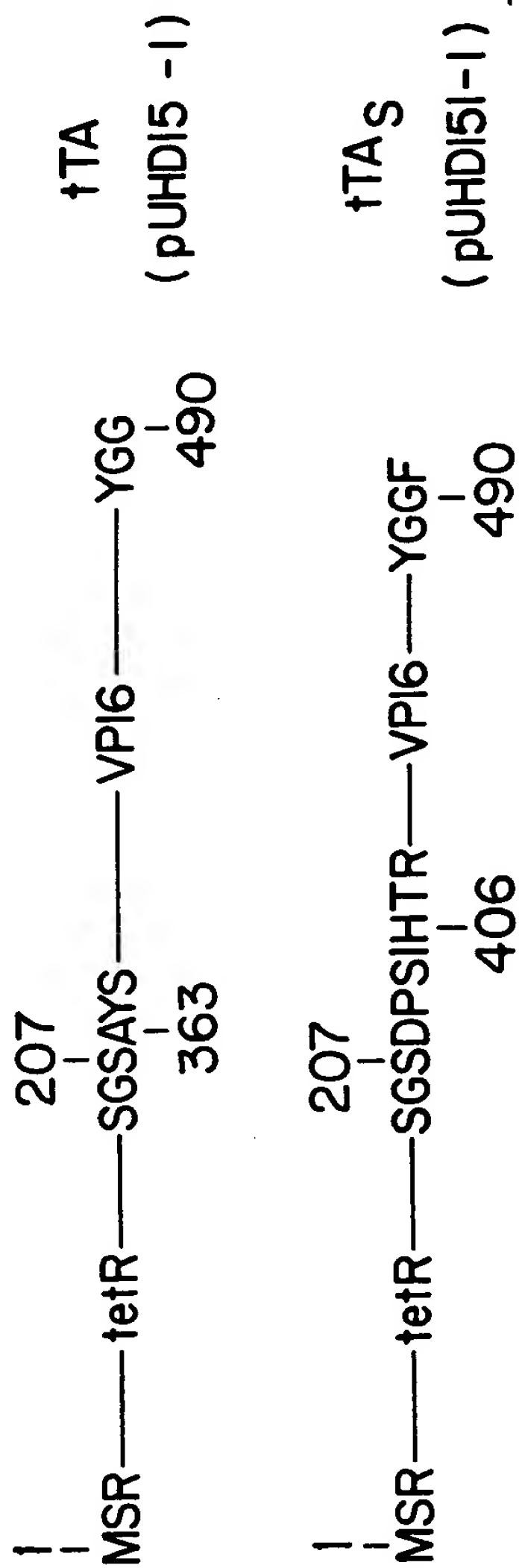
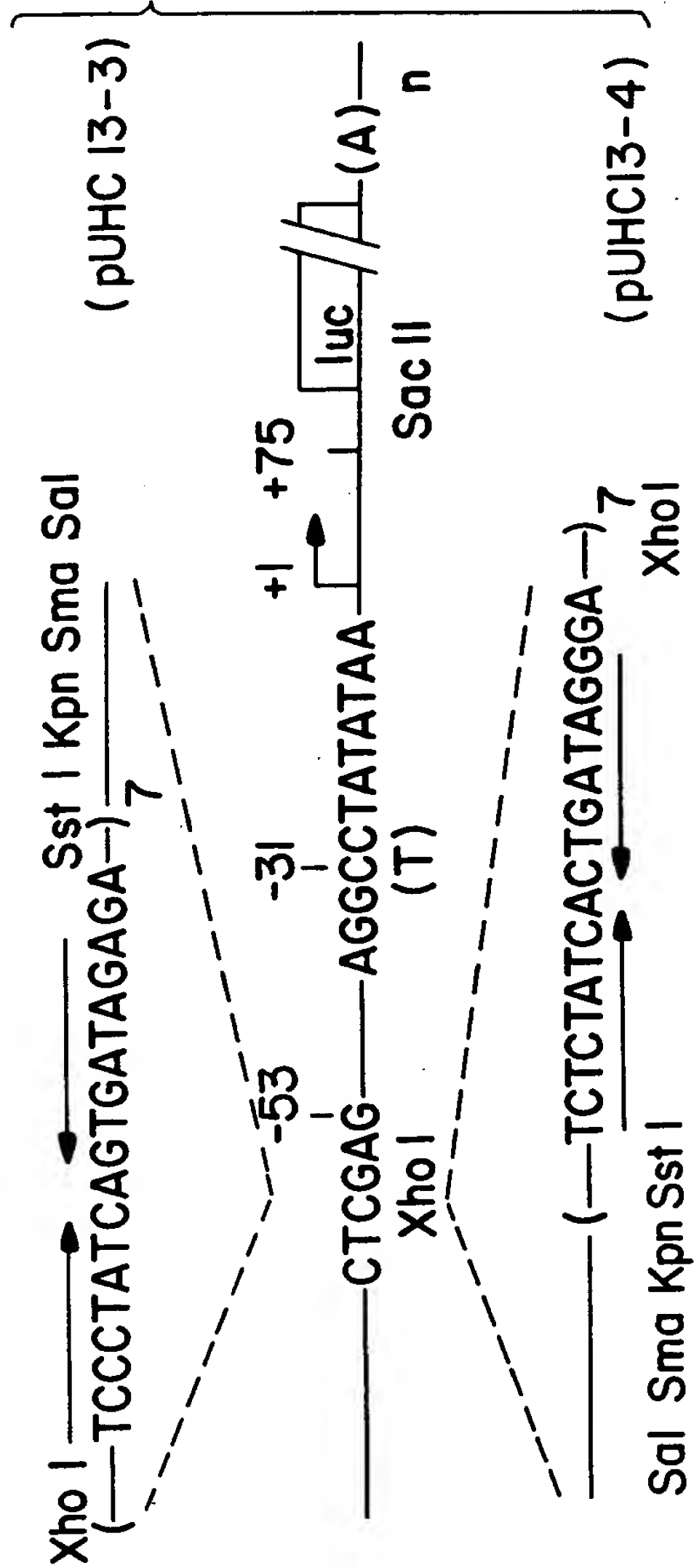
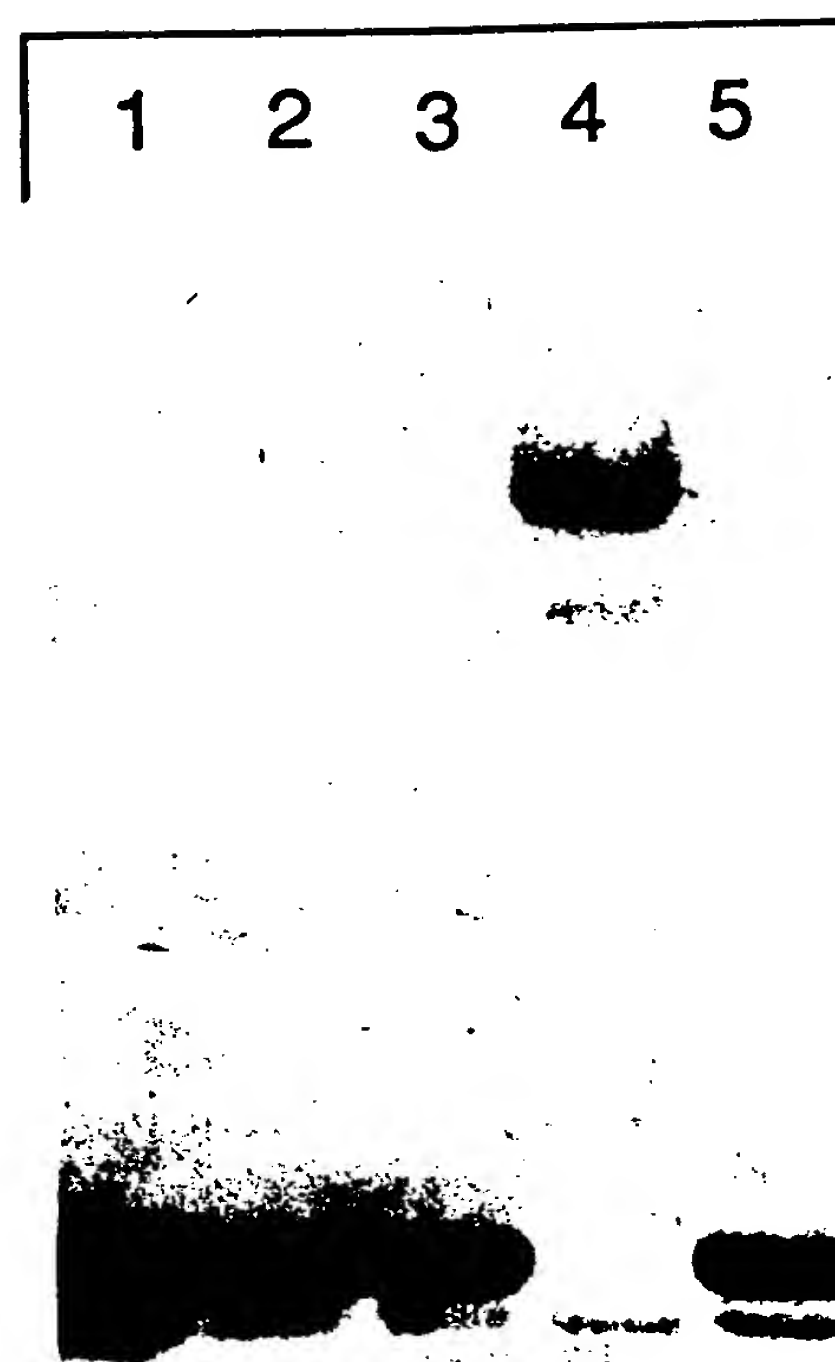
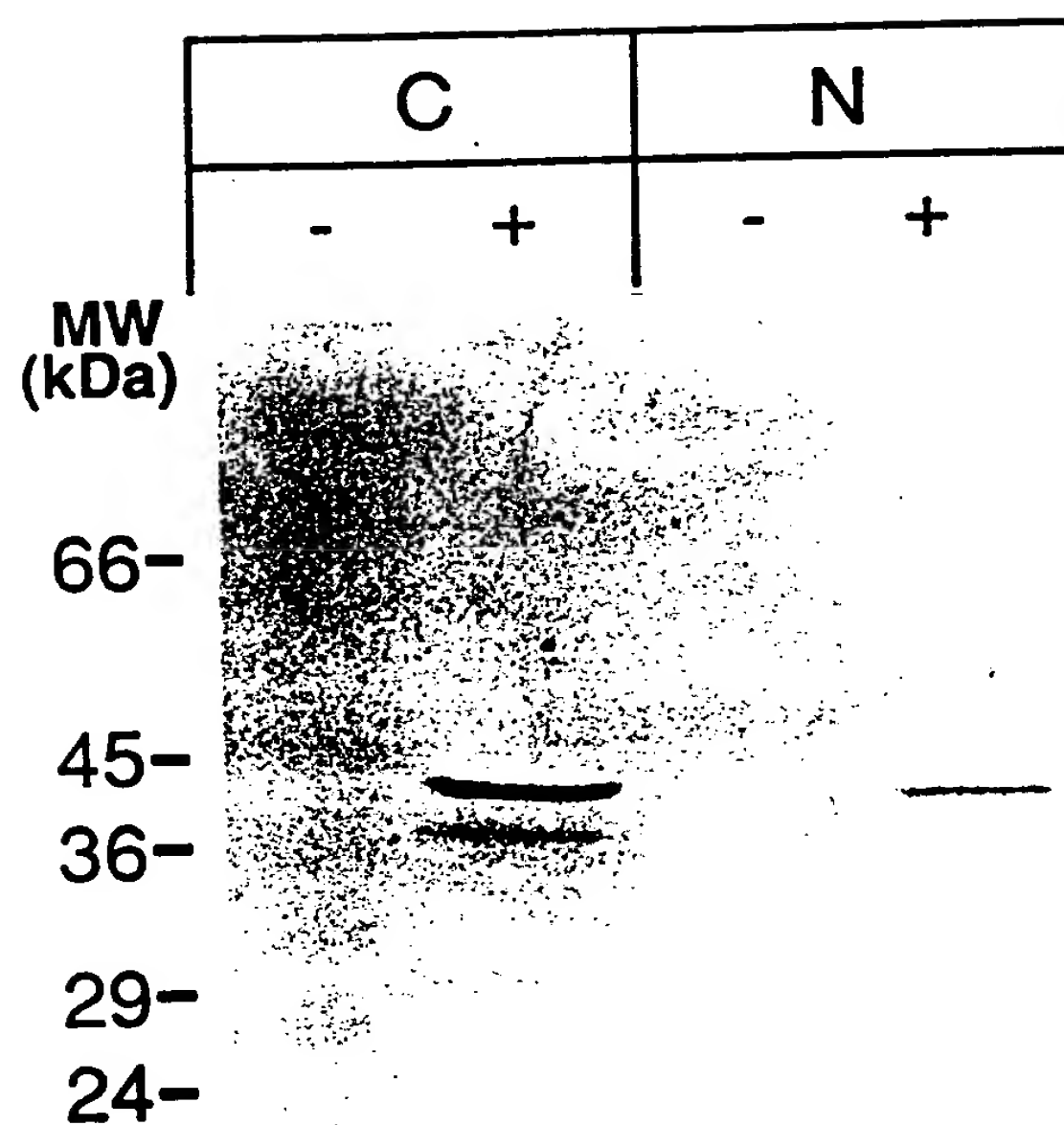


FIG. 1A



F/G/B





660600-42378200

FIG. 3A

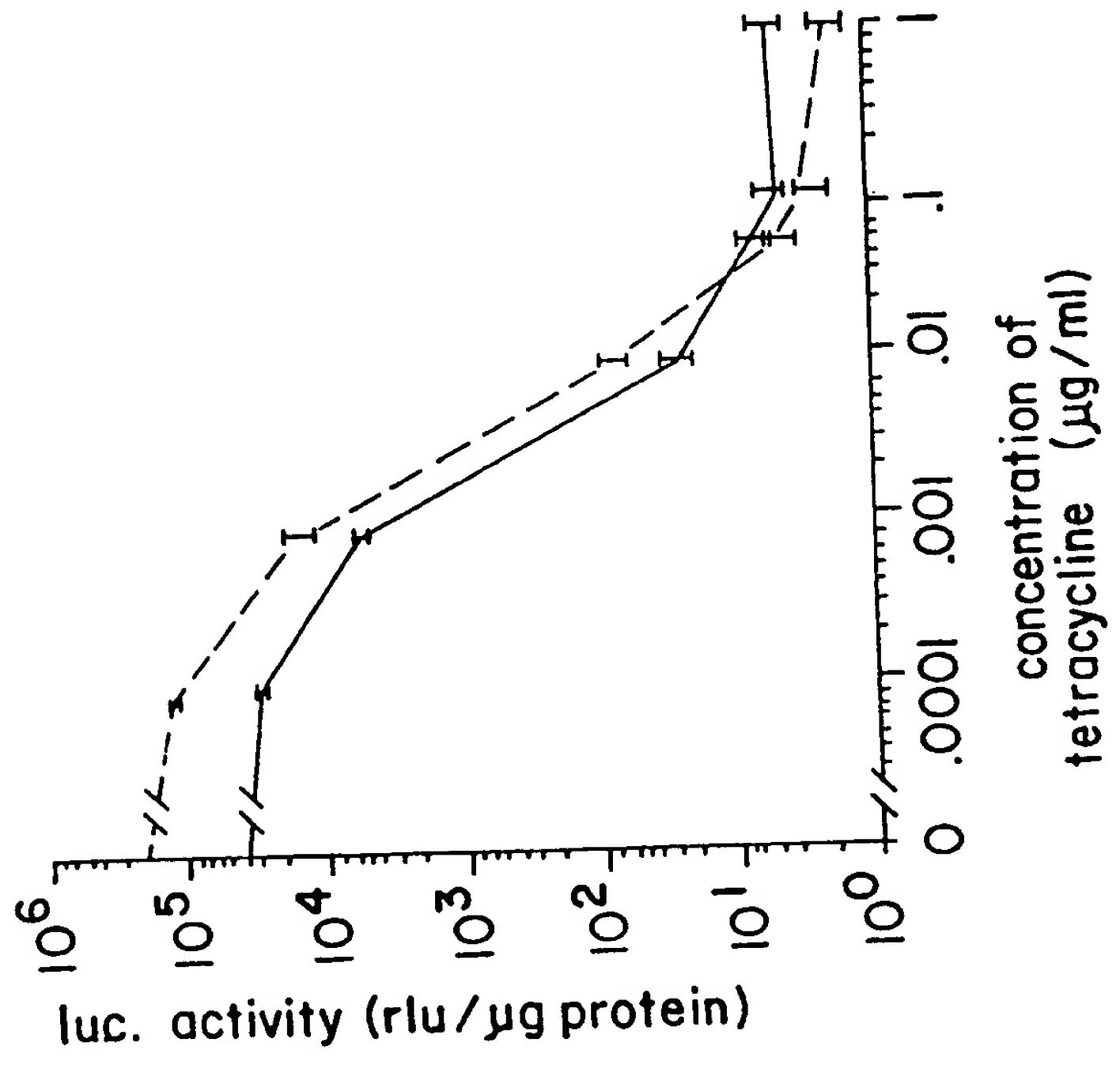
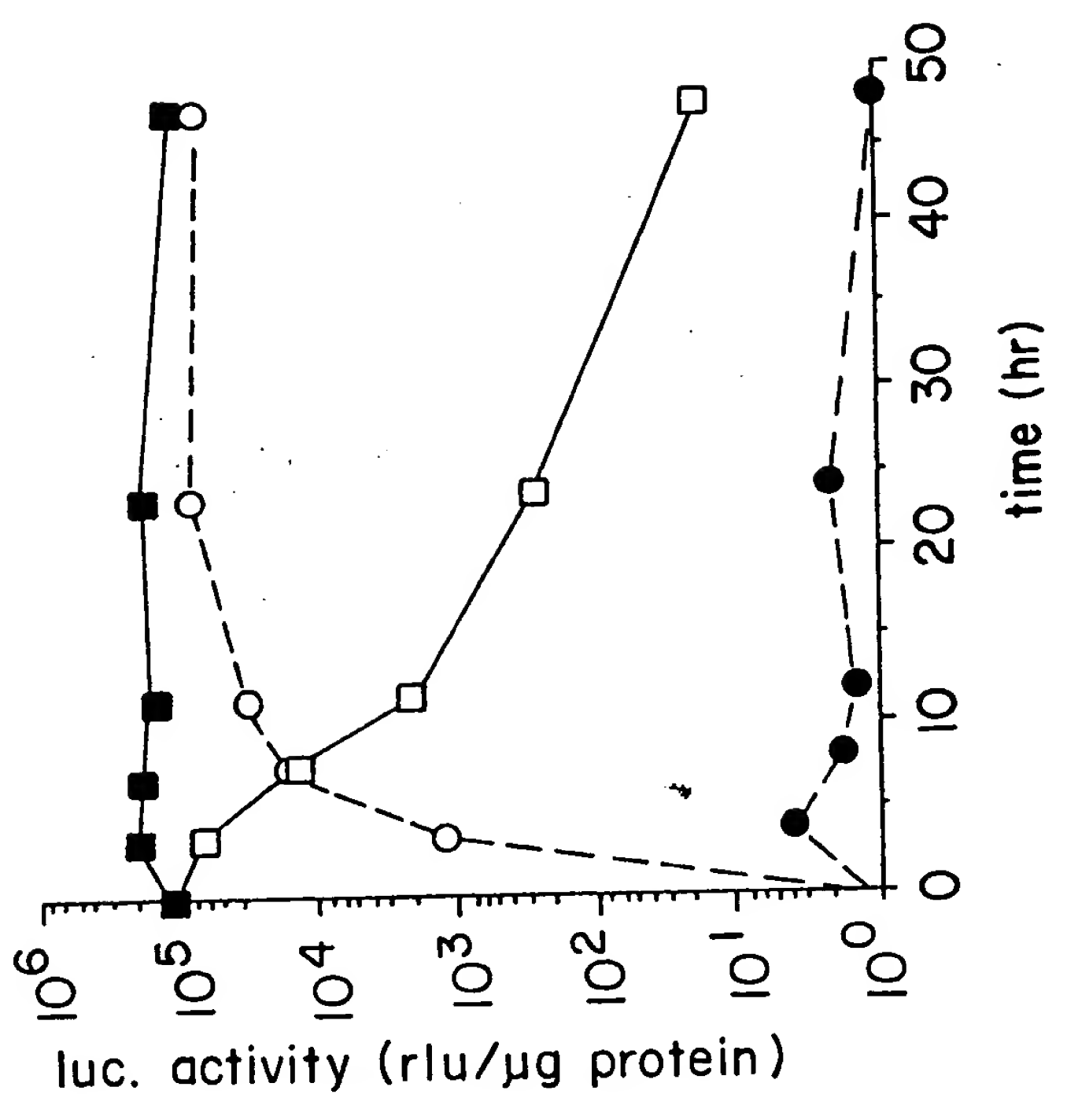


FIG. 3B



5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

CTA	AGT	CAT	CGC	GAT	GGA	GCA	AAA	GTA	CAT	TTA	GGT	ACA	CGG	CCT	ACA	GAA	AAA
Leu	Ser	His	Arg	ASP	Gly	Ala	Lys	Val	His	Leu	Gly	Thr	Arg	Pro	Thr	Glu	Lys
CAG	TAT	GAA	ACT	CTC	GAA	AAT	CAA	TTA	GCC	TTT	TTA	TGC	CAA	CAA	GGT	TTT	TCA
Gln	Tyr	Glu	Thr	Leu	Glu	Asn	Gln	Leu	Ala	Phe	Leu	Cys	Gln	Gln	Gly	Phe	Ser
CTA	GAG	AAT	GCA	TTA	TAT	GCA	CTC	AGC	GCT	GTG	GGG	CAT	TTT	ACT	TTA	GGT	TGC
Leu	Glu	Asn	Ala	Leu	Tyr	Ala	Leu	Ser	Ala	Val	Gly	His	Phe	Thr	Leu	Gly	Cys
GTA	TTG	GAA	GAT	CAA	GAG	CAT	CAA	GTC	GCT	AAA	GAA	GAA	AGG	GAA	ACA	CCT	ACT
Val	Leu	Glu	Asp	Gln	Glu	His	Gln	Val	Ala	Lys	Glu	Glu	Arg	Glu	Thr	Pro	Thr
ACT	GAT	AGT	ATG	CCG	CCA	TTA	TTA	CGA	CAA	GCT	ATC	GAA	TTA	TTT	GAT	CAC	CAA
Thr	Asp	Ser	Met	Pro	Pro	Leu	Leu	Arg	Gln	Ala	Ile	Glu	Leu	Phe	Asp	His	Gln

Fig. 4B

AAA	CAA	CTT	AAA	TGT	GAA	AGT	GGG	TCC	GCG	TAC	AGC	CGC	GCG	CGT	ACG	AAA	AAC
Lys	Gln	Leu	Lys	Cys	Glu	Ser	Gly	Ser	Ala	Tyr	Ser	Arg	Ala	Arg	Thr	Lys	Asn

AAT	TAC	GGG	TCT	ACC	ATC	GAG	GGC	CTG	CTC	GAT	CTC	CCG	GAC	GAC	GCC	CCC
Asn	Tyr	Gly	Ser	Thr	Ile	Glu	Gly	Leu	Leu	Asp	Leu	Pro	Asp	Asp	Ala	Pro

GAA	GAG	GCG	GGG	CTG	GCG	GCT	CCG	CGC	CTG	TCC	TTT	CTC	CCC	GCG	GGA	CAC	ACG
Glu	Glu	Ala	Ala	Gly	Leu	Ala	Pro	Arg	Leu	Ser	Phe	Leu	Pro	Ala	Gly	His	Thr

CGC	AGA	CTG	TCG	ACG	GCC	CCC	CCG	ACC	GAT	GTC	AGC	CTG	GGG	GAC	GAG	CTC	CAC
Arg	Arg	Leu	Ser	Thr	Ala	Pro	Pro	Thr	Asp	Val	Ser	Leu	Gly	Asp	Glu	Leu	His

Fig. 4C

Sequence of the gene

TTA GAC GGC GAG GAC GTG GCG ATG GCG CAT GCC GAC GCG CTA GAC GAT TTC GAT
 Leu Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp

CTG GAC ATG TTG GGG GAC GGG GAT TCC CCG GGT CCG GGA TTT ACC CCC CAC GAC
 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His Asp

TCC GCC CCC TAC GGC GCT CTG GAT ATG GCC GAC TTC GAG CAG ATG TTT
 Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Gln Met Phe

ACC GAT CCC CTT GGA ATT GAC GAG TAC GGT GGG TAG
 Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly *

Fig. 4D

[illegible]

ATG	TCT	AGA	TTA	GAT	AAA	AGT	AAA	GTG	ATT	AAC	AGC	GCA	TTA	GAG	CTG	CTT	AAT
Met	Ser	Arg	Leu	Asp	Lys	Ser	Lys	Val	Ile	Asn	Ser	Ala	Leu	Glu	Leu	Leu	Asn

GAG	GTC	GGA	ATC	GAA	GGT	TTA	ACA	ACC	CGT	AAA	CTC	GCC	CAG	AAG	CTA	GGT	GTA
Glu	Val	Gly	Ile	Glu	Gly	Leu	Thr	Thr	Arg	Lys	Leu	Ala	Gln	Lys	Leu	Gly	Val

GAG	CAG	CCT	ACA	TTG	TAT	TGG	CAT	GTA	AAA	AAT	AAG	CGG	GCT	TTG	CTC	GAC	GCC
Glu	Gln	Pro	Thr	Leu	Tyr	Trp	His	Val	Lys	Asn	Lys	Arg	Ala	Leu	Leu	Asp	Ala

TTA	GCC	ATT	GAG	ATG	TTA	GAT	AGG	CAC	CAT	ACT	CAC	TTT	TGC	CCT	TTA	GAA	GGG
Leu	Ala	Ile	Clu	Met	Leu	Asp	Arg	His	His	Thr	His	Phe	Cys	Pro	Leu	Glu	Gly

GAA	AGC	TGG	CAA	GAT	TTT	TTA	CGT	AAT	AAC	GCT	AAA	AGT	TTT	AGA	TGT	GCT	TTA
Glu	Ser	Trp	Gln	Asp	Phe	Leu	Arg	Asn	Asn	Ala	Lys	Ser	Phe	Arg	Cys	Ala	Leu

Fig. 5A

CTA AGT CAT CGC GAT GGA GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA
Leu Ser His Arg Asp Gly Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys

CAG TAT GAA ACT CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA
Gln Tyr Glu Thr Leu Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser

CTA GAG AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC
Leu Glu Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys

GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA CCT ACT
Val Leu Glu Asp Gln Gln His Glu Val Ala Lys Glu Glu Arg Glu Thr Pro Thr

ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA TTT GAT CAC CAA
Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu Phe Asp His Gln

Fig. 5B

GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG ATC ATA TGC GGA TTA GAA
Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Glu Ile Cys Gly Leu Glu

AAA	CAA	CTT	AAA	TGT	GAA	AGT	GGG	TCT	GAT	CCA	TCG	ATA	CAC	ACG	CGC	AGA	CTG
Lys	Gln	Leu	Lys	Cys	Glu	Ser	Gly	Ser	Asp	Pro	Ser	Ile	His	Thr	Arg	Arg	Leu

TCG	ACG	GCC	CCC	CCG	ACC	GAT	GTC	AGC	CTG	GGG	GAC	GAG	CTC	CAC	TTA	GAC	GGC
Ser	Thr	Ala	Pro	Pro	Thr	Asp	Val	Ser	Leu	Gly	Asp	Glu	Leu	His	Leu	Asp	Gly

GAG GAC GTG GCG ATG GCG CAT GCC GAC GCG CTA GAC GAT TTC GAT CTG GAC ATG
Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Phe Asp Leu Asp Met

TTG	GGG	GAC	GGG	GAT	TCC	CCG	GGT	CCG	CCG	TTT	ACC	CCC	CAC	GAC	TCC	GCC	CCC
Leu	Gly	Asp	Gly	Asp	Ser	Pro	Gly	Pro	Gly	Phe	Thr	Pro	His	Asp	Ser	Ala	Pro

Fig. 5C

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

TAC GGC GCT CTG GAT ATG GCC GAC TTC GAG TTT GAG CAG ATG TTT ACC GAT GCC
 Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu Gln Met Phe Thr Asp Ala

CTT GGA ATT GAC GAG TAC GGT GGG TTC TAG
 Leu Gly Ile Asp Glu Tyr Gly Gly Phe *

Fig 5D

Sequence 1

GAATTCCCTCGAGTTTACCACCTCCCTATCAGTGATAGAGAAAGTGAAAGTCGAGTTTACCACCTC
CCTATCAGTGATAGAGAAAGTGAAAGTCGAGTTTACCACCTCCCTATCAGTGATAGAGAAAGT
GAAAGTCGAGTTTACCACCTCCCTATCAGTGATAGAGAAAGTGAAAGTCGAGTTTACCACCTCCC
TATCAGTGATAGAGAAAGTGAAAGTCGAGTTTACCACCTCCCTATCAGTGATAGAGAAAGTGA
AAGTCGAGTTTACCACCTCCCTATCAGTGATAGAGAAAGTGAAAGTCGAGTCGGTACCCGGGT
CGAGTAGGCGTGACGGTGGGAGGCCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGC
CTGGAGACGCCATCCACGCTGTTTGGACCTCCATAGAAGACACCGGACCGATCCAGCCTCCGC

GG

Fig. 6

Fig. 7

Fig. 8

CTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATC
 AGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGT
 CGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATCAG
 TGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCG
 AGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGCTCGGTACCCGGGTCGAGTA
 GGCGTGTA CGGTGGGAGGCCATATAAGCAGAGCTCGTTTAGTGAAACCGTCAGATCGCCTGGAG
 ACGCCATCCACGCTGTTTGACCTCCATAGAGACACCGGACCGATCCAGCCTCCGCGGCCCC
 GAATTCGAGCTCGGTACCGGGCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATCGAAT
 TCCAGGAGGTGGAGATCCGCGGTCCAGCCAAACCCACACCAATTTTCTCCTCCCTCTGCCCC
 TATATCCCGGCACCCCTCCTCCTAGCCCTTTCCCTCCTCCGAGAGACGGGGAGGAGAAAAG
 GGGAGTTT'AGGTCGACATGACTGAGCTGAAGGCAAGGAACCTCGGGCTCCCCACGTGGCGGGC
 GCGCGCCCTCCCCACCGAGGTCGGATCCCAGCTCCTGGGTGCGCCCGGACCCCTGGCCCCCTCC
 AGGGGAGCCAGACCTCAGAGGCCCTCGTCTGTAGTCTCGCCATCCCCATCTCCCTGGACGGGTT

Fig. 9A

SECRET

GCTCTTCCCCGGCCCTGT CAGGGGCAGAACCCCCAGACGGGAAGACGCAGGACCCACCGTCCG
TTGTCAGACGTGGAGGGCGCATTTCTTGAGTTCGAAGCCCCGGAGGGGCAGGAGACAGCAGCT
CGAGACCTCCAGAAAGGACAGCGGCCCTGCTGGACAGTGTCTCGACACGCTCCTGGCGCCCTC
GGTCCCGGCAGAGCCACGCCAGCCCTGCCACCTGCGAGGCCATCAGCCCCTGCTGCTGCTCA
GGCCCCGACCTTCCCGAAGACCCCCGGGCTGCCCCCGCTACCAAAGGGTGTGGCCCCCGCTCA
TGAGCCGACCCGAGGACAAGGCAGCGCACAGCTCTGGGACGGCAGCGGCCCAAGGTGCTGCC
CAGGGACTGTCACCATCCAGGCAGCTGCTGCTCCCCCTCTGGGAGCCCTCACTGGCCCCGCA
GTGAAGCCATCCCCGAGCCCGCTGCGGTGCAGGTAGACGAGGAGACAGCTCCGAATCCGAGG
GCACCGTGGGCCCGCTCCTGAAGGCCAACCTCGGGCACTGGGAGGCACGGCGGCCGAGGAGG
AGCTGCCCCCGTCCGTCTGGAGCGGCCGCAGGAGCGTCCCTTGTCCCCAAGGAAGATTCT
CGCTTCTCGGCGCCAGGGTCTCCTTGGCGGAGCAGGACGCGCCGTGGCGCTGGCGCTCCC
CGCTGGCCACCTCGGTGGTGATTTCATCCACGTGCCCATCCTGCCCTCTCAACCACGCTTTCCT
GGCCACCCGCACCGCAGCTGCTGGAGGGGAGAGCTACGACGGCGGGCCGCGGCCGCGCAGC

Fig. 9B

4431320

CCCTTCG¹CCCCGACGGGGCTCCCCCTCTGCTCCTCGTCCACCCCTGTGGCGGGCGGCGACTTCC
CCGACTGCACCTACCCGCCGACGCCGAGCCCAAGATGACGCGTTCCCCCTCTACGGCGACTT
CCAGCCGCCGCCCTCAAGATAAAGGAGGAGGAAGAGCCGCCGAGGCCGCGCGCTCCCCCG
CGTACGTACCTGGTGGCTGGTGCAAAACCCGCCCTTCCGGACTTCCAGCTGGCAGCGCCGC
CGCCACCTCGCTGCCGCCCTCGAGTGCCCTCGTCCAGACCCGGGAAGCGCGGTGGCGGCCTC
CCCAGGCAGTGCCCTCCGTCTCCTCGTCCCTCGTCCGGGTGACCCCTGGAGTGCAATCCTGTAC
AAGGCAGAGCGCGGCCGCCAGCAGGGCCCCCTTCGCGCCGCTGCCCTGCAAGCCTCCGGGCG
CCGGCGCCTGCTGCTCCCGCGGACGGCCTGCCCTCCACCTCCGCCCTCGGGCGCAGCCGCCGG
GGCCGCCCTGCGCTCTACCCGACGCTCGGCCCTCAACGGACTCCCGCAACTCGGCTACCAGGCC
GCCGTGCTCAAGGAGGGCCTGCCGAGGTCTACAGCCCTATCTCAACTACCTGAGGCCGGATT
CAGAAGCCAGTCAGAGCCACAGTACAGCTTCGAGTCACTACCTCAGAAGATTGTGATCTG
TGGGGATGAAGCATCAGGCTGTCAATTATGGTGTCCTCACCTGTGGAGCTGTAAAGTCTTCTTT
AAAAGGCAATGGAAGGGCAGCATAACTATTTATGTGCTGGAAGAAATGACTGCATTGTTGATA

Fig. 9C

AAATCCGCAGGAAAACTGCCCGGCGTGTAGAAAGTGCTGTCAAGCTGGCATGGTCCT
 TGGAGGGCGAAAGTTTAAAAAGTTCAATAAAGTCAGAGTCATGAGAGCACTCGATGCTGTGCT
 CTCCACAGCCAGTGGGCATTCCAAATGAAAGCCAAAGCAATCACTTTTCTCCAAGTCAAGAGA
 TACAGTTAATTCCCCCTCTAATCAACCCTGTTAATGAGCATTTGAACCAGATGTGATCTATGCAGG
 ACATGACAAACAAAGCCTGATACCTCCAGTCTTTGCTGACGAGTCTTAATCAACTAGCGGAG
 CGGCAACTTCTTCAGTGGTAAATGGTCCAAATCTCTTCCAGGTTTTCGAAACTTACATATTG
 ATGACCAGATAACTCTCATCCAGTATTCTTGGATGAGTTTAATGGTATTTGGACTAGGATGGAG
 ATCCTACAAACATGTCAGTGGGCAGATGCTGTATTTTGCACCTGATCTAATATTAATGAACAG
 CGGATGAAAGAAATCATCATCTATTCATACTATGCCCTTACCATGTGGCAGATACCGCAGGAGTTTG
 TCAAGCTTCAAGTTAGCCAAGAGAGTTCCCTGCAATGAAGTATTACTTCTTAATACAAT
 TCCTTTTGAAGGACTAAGAAAGTCAAAGCCAGTTTGAAGAGATGAGATCAAGCTACATTAGAGAG
 CTCATCAAGGCAATTGGTTTGAGGCAAAAGGAGTTGTTTCCAGCTCACAGCGTTTCTATCAGC
 TCACAAAACCTTCTTGATAACTTGCATGATCTTGTCAAACAACCTTCACCTGTACTGCCCTGAATAC

Fig. 9D

ATTATCCAGTCCCGGCGCTGAGTGTGAATTTCCAGAAATGATGTCTGAAGTTATTGCTGCA
CAGTTACCCAAGATATTGGCAGGATGGTGAAACCACTTCTCTTTCATAAAAAGTGAATGTCAA
TTATTTTCAAAGAATTAAAGTGTGTGGTATGTCTTTTGGTCAGGATTATGACGTCTCG
AGTTTTTATAATATTCTGAAAGGAATTCCTGCAGCCCCGGGATCCACTAGTTCTAGAGGATC
CAGACATGATAAGATACATTGATGAGTTTGGACAAACCACTAGAAATGCAGTGAAAAAATG
CTTATTTGTGAAATTTGTGATGCTATTGCTTTATTGTAAACCATTAATAAGCTGCAATAAACAA
GTTAACAAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGAGGTGTGGAGGTTTTTT
AAAGCAAGTAAACCTCTACAAATGTGTATGGCTGATTATGATCCTGCAAGCCTCGTCGTCTG
GCCGGACCACGCTATCTGTGCAAGGTCCCCGGACGCGCTCCATGAGCAGAGCGCCCGCCGCC
GAGGCAAGACTCGGGCGGCCCTGCCCCGTCCACCAAGGTCAACAGGCGGTAAACCGGCTCTTC
ATCGGGAATGCGCGCACCTTCAGCATCGCCGGCATGTCCCCTGGCGGACGGGAAGTATCAGCT
CGACCAAGCTTGGCGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAAAAAATCACTGGAT
ATACCACCGTTGATATATCCCAATGGCATCGTAAGAACAATTTTGAGGCATTTTCAGTCAGTTGC

Fig. 9E

TCAATGTACCTATAACAGACCGTTTCAGCTGCATTAAATGAATCGCCAAACGCGGGGAGAGGC
GGTTTGGGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCTCGTTCGGC
TGCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAAATCAGGGGATAA
CGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTG
CTGGCGTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAATAATCGACGCTCAAAGTCAGA
GGTGGCAACCCGACAGGACTATAAAGATACAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCG
CTCTCCTGTTCCGACCCCTGCCGCTTACCGGATACCTGTCCGCCCTTCTCCCTTCGGGAAGCGTG
GGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGTCTGTTCCGCTCCAAGCTGG
GCTGTGACGAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGA
GTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA
GCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAAGTGGTGGCCTAACTACGGCTACACTAGAA
GGACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTC
TTGATCCGGCAAAACCAACCGCTGGTAGCGGTGTTTTTTTGTGTTGCAAGCAGCAGATTACG

Fig. 9F

CGCAGAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGA
 ACGAAAACTCACGTTAAGGATTTTGGTCATGAGATTATCAAAAAGGATCTTACCTAGATCCT
 TTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATAGTAATAACTTGGTCTGACAGT
 TACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTG
 CCTGACTCCCCGTCGTAGATAAATACTACGATACGGAGGGCTTACCATCTGGCCCCAGTGCTGC
 AATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTATCAGCAATAAACAGCCAGCCGGA
 AGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCCTCCAGTCTATTAATTGTTGCC
 GGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTGTCATTGCTACAGG
 CATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTACAGCTCCGGTTCCTCAACGATCAAGG
 CGAGTTACATGATCCCCCATGTTGTGCAAAAAGCGTTAGCTCCTTCGGTCTCCGATCGTTG
 TCAGAAGTAAGTTGGCCGAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTAC
 TGTGATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAA
 TAGTGATGCGGCGACCGAGTTGCTCTTGCCCCGGCGTCAATACGGGATAATACCGGCCACATA

Fig. 9G

GCAGAACTTTAAAGTGCTCATCTTGGAACAAGTTCTTCGGGGCGAAAACTCTCAAGGATCTT
ACCGCTGTTGAGATCCAGTTCGATGTAAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTT
ACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAA
GGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTCAATATTAATTGAAGCATTTATCA
GGGTTATTGTCTCATGAGCGGATACATATTGAATGTATTTAGAAAATAAAACAAATAGGGGTT
CCGCGCACATTTCCCCGAAAGTGCCACCCTGACGCTCTAGAAACCATTATTATCATGACATTAA
CCTATAAAATAGGCGTATCAGAGGCCCTTTTCGTC

Fig. 9H

1997 年 12 月 31 日 止
 1997 年 12 月 31 日 止

CTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACCTCCCTATC
AGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACCTCCCTATCAGTGATAGAGAAAAGTGAAAGT
CGAGTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACCTCCCTATCAG
TGATAGAGAAAAGTGAAAGTCGAGTTTACCACCTCCCTATCAGTGATAGAGAAAAGTGAAAGTCCG
AGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACCTCCCTATCAGTA
GGCGTGACGGTGGGAGGCCCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAG
ACGCCATCCA CGCTGTTT TGACCTCCATAGAGACACCGGACCGATCCAGCCTCCGCGGCCCC
GAATTCCGCCACGACCATGACCATGACCTCCACACCAAGCATCTGGATGGCCCTACTGCA
TCAGATCCAAGGAACGAGCTGGAGCCCCTGAACCGTCCGCAGCTCAAGATCCCCCTGGAGCGG
CCCCTGGGCAGGTGTACCTGGACAGCAAGCCCGCGTGTACAACCTACCCGAGGCGCCG
CCTACGAGTTCAACGCCGCGCGCCGCAACGCCAGGTCTACGGTCAGACCGGCTCCCCCTA
CGCCCCGGGTCTGAGGCTGCGGCGTTTCGGCTCCAACGGCCTGGGGGTTTCCCCCCTCAAC
AGCGTGCTCCGAGCCGCTGATGCTACTGCACCCGCCCGCAGCTGTGCCCTTCTCCTGCAGC

Fig. 10A

CCCACGGCCAGCAGGTGCCCTACTACCTGGAGAACGAGCCAGCGGCTACACGGTGCGCGAGGC
CGGCCCGCGGCATTCTACAGGCCAAATTCAGATAATCGACGCCAGGGTGGCAGAGAAAGATTG
GCCAGTACCAATGACAAAGGAAGTATGGCTATGGAATCTGCCAAGGAGACTCGCTACTGTGCAG
TGTGCAATGACTATGCTTCAGGCTACCATTAATGGAGTCTGGTCTGTGAGGGCTGCAAGGCCTT
CTTCAAGAGAAGTATTCAAGGACATAACGACTATATGTGTCCAGCCACCAACCAGTGCACCATTT
GATAAAACAGGAGGAAGAGCTGCCAGGCCCTGCCGGCTCCGCAAAATGCTACGAAGTGGGAATGA
TGAAAGGTGGGATACGAAAAGACCGAAGAGGAGGGAGAATGTTGAAACACAAGCGCCAGAGAGA
TGATGGGAGGCGAGGGTGAAAGTGGGTCTGCTGGAGACATGAGAGCTGCCAACCTTTGGCCA
AGCCCGCTCATGATCAAACGCTCTAAGAAGAACAGCCTGGCCTTGTCCTGACGGCCGACCAGA
TGGTCATGGCCTTGTTGGATGCTGAGCCCCCATACTCTATTCCGAGTATGATCCTACCAGACC
CTTCAGTGAAGCTTCGATGATGGGCTTACTGACCAACCTGGCAGACAGGAGCTGGTTCACATG
ATCAACTGGCGAAGAGGGTGCCAGGCTTTGTGGATTTGACCCCTCCATGATCAGGTCCACCTTC
TAGAATGTGCTGGCTAGAGATCCTGATGATTGGTCTCGTCTGGCGCTCCATGGAGCACCCAGT

Fig. 10B

GAAGCTACTGTTTGTCTCCTAACTTGTCTCTTGGACAGGAACCCAGGAAATGTGTAGAGGGCATG
GTGGAGATCTTCGACATGCTGCTGGCTACATCATCTCGGTTCCGCATGATGAATCTGCAGGGAG
AGGAGTTTGTGTGCCCTCAAATCTATTATTTTGCTTAATTCTGGAGTGTAACATTTCTGTCCAG
CACCCCTGAAGTCTCTGGAAGAGAAGACCATAATCCACCGAGTCTTGACAAGATCACAGACACT
TTGATCCACCTGATGGCCAAGGCAGGCCCTGACCCCTGCAGCAGCACCGCGGCTGGCCCAGC
TCCTCCTCATCCTCTCCCACATCAGGCACATGAGTAACAAGGCATGGAGCATCTGTACAGCAT
GAAGTGCAAGAACGTGGTGCCCTCTATGACCTGTCTGGAGATGCTGGACGCCACCGCCTA
CATGCGCCCACTAGCCGTGGAGGGCATCCGTGGAGGAGACGGACCAAAGCCACTTGGCCACTG
CGGGCTCTACTTCATCGCATTCCTTGCAAAAGTATTACATCACGGGGGAGGCAGAGGGTTTCCC
TGCCACAGTCTGAGAGCTCCCTGGCGGAATTTCGAGCTCGGTACCCGGGGATCCTCTAGAGGATC
CAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATG
CTTTATTTGTGAAATTGTGATGCTATTGCTTTTATTGTAAACCATTAAGCTGCAATAAACA
GTTAAACAACAATTGCATTCTTTATGTTTCAGGTTCAGGGGAGGTGTGGGAGGTTTTTTT

Fig. 10C

[illegible]

AAAGCAAGTAAACCTCTACAAATGTGGTATGGCTGATTATGATCCTGCAAGCCTCGTCGTCCTG
GCCGGACCACGCTATCTGTGCAAGGTCCCGGACGCGCTCCATGAGCAGAGCGCCCGCCGCC
GAGGCAAGACTCGGGCGGCCCTGCCCTGCCAGGTCAACAGGCGGTAAACCGGCCTCTTTC
ATCGGGAATGCGCGGACCTTTCAGCATCGCCGGCATGTCCCCTGGCGGACGGGAAGTATCAGCT
CGACCAAGCTTGGCGAGATTTTCAGGAGCTAAGGAAGCTAAATAATGGAGAAAATACTACTGGAT
ATACCACCGTTGATATATCCCAATGGCATCGTAAGAACAATTTTGAGGCATTTTCAGTCAGTTGC
TCAATGTACCTATAACCAGACCGTTTCAGCTGCATTAATGAATCGGCCAACGCGGGGAGAGGC
GGTTTGCGTATTGGGCGCTCTTCCGCTTCCGCTCACTGACTCGCTCGCTCGGTCGTTTCGGC
TGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAA
CGCAGGAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAGCCGCGTTG
CTGGCGTATTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGA
GGTGGCAAACCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAAGCTCCCTCGTGCG
CTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG

Fig. 10D

660600 44343260

GCGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGG
GCTGTGTGCAGAACCCCGTTTCAGCCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGA
GTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA
GCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAA
GGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTC
TTGATCCC GCAAAACAAACCACCGCTGGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATTACG
CGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGGA
ACGAAAACTCACGTTAAGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCT
TTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATAGATAAATTTGGTCTGACAGT
TACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTCCATCCTAGTTG
CCTGATCCCCGTGCTAGATAACTACGATACGGAGGGCTTACCATCTGGCCCCAGTGCTGCA
ATGATACCGGAGACCCACGCTCACCGGCTCCAGATTATCAGCAATAAACAGCCAGCCGGAA
GGGCCGAGCGAGAAGTGGTCCTGCAACTTATCCGCTCCATCCAGTCTATTAATTGTTGCCG

Fig. 10E

11-11-55

GGAAGCTAGTAAGTAGTTCGCCAGTTAATAGTTTGCACAACGTTGTTGCCATTGCTACAGGC
ATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTACAGCTCCGGTTCCTCCGATCGTTGT
GAGTTACATGATCCCCCATGTTGTGCAAAAAGCGTTAGCTCCTTCGGTCCCTCCGATCGTTGT
CAGAAGTAAGTTGGCCGAGTGTTATCACTCATGCTTATGGCAGCACTGCATAATTCTCTTACT
GTCA TGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAAT
AGTGATGCGGCACCGAGTTGCTCTTGCCCCGGCTCAATACGGGATAATACCGCCACATAG
CAGAACTTTAAAAGTGCTCATCATTTGGAACAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTA
CCGCTGTTGAGATCCAGTTCGATGTAAACCCACTCGTGCAACCCTGATCTTCAGCATCTTTTA
CTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAG
GGCGACACGGAAATGTTGAATACTCATACTCTTCCCTTTTCAATAATTATTGAAGCATTTATCAG
GGTTATTGCTCATGAGCGGATACATATTGAAATGTATTTAGAAAAATAACAATAGGGGTTTC
CGCGCACATTTCCCCGAAAAGTGCCACCTGACGCTAAGAAACCATTTATTCATGACATTAAAC
CTATAAAAATAGCGGTATCACGAGGCCCTTTCGTC

Fig. 10F

FIG. 11

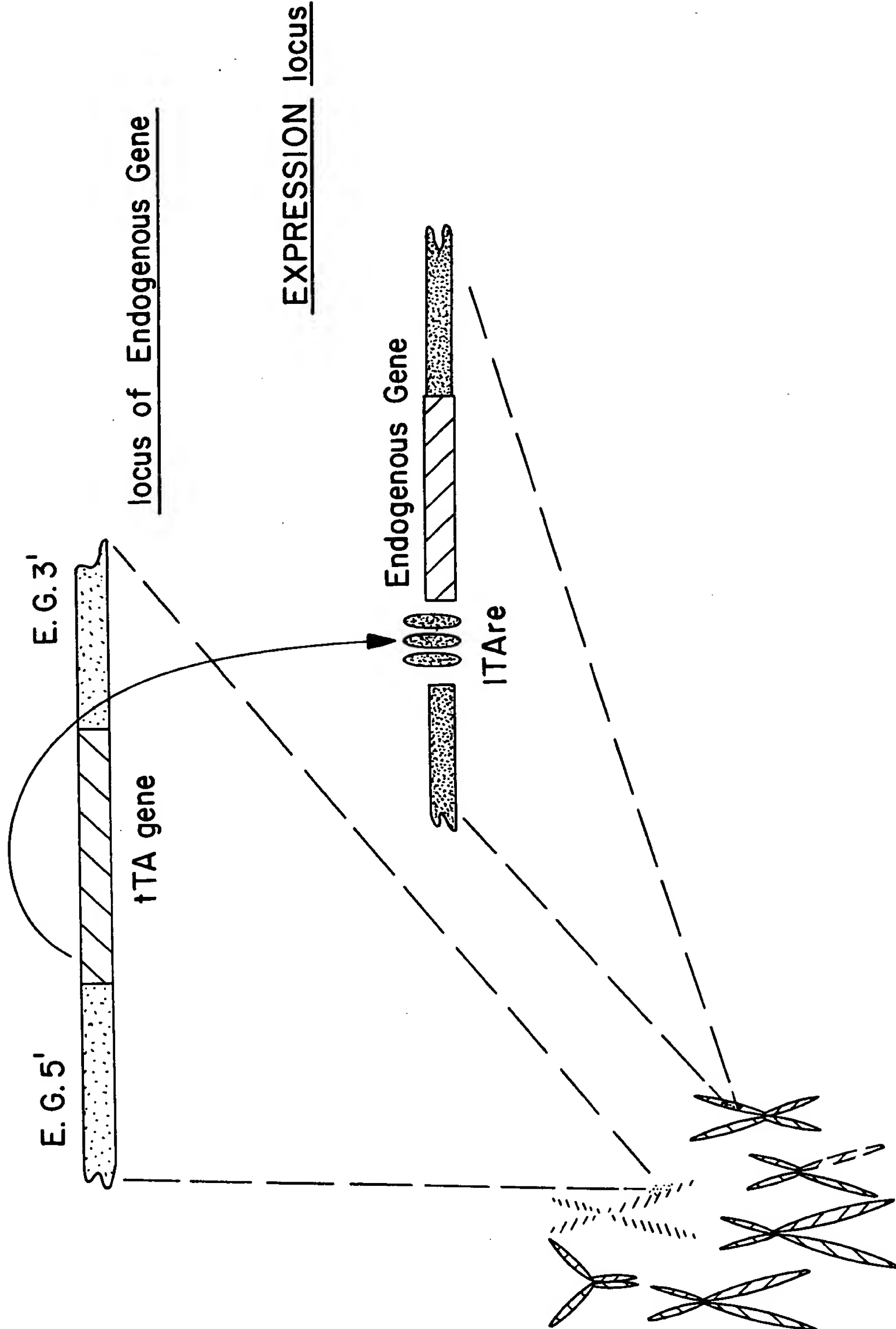
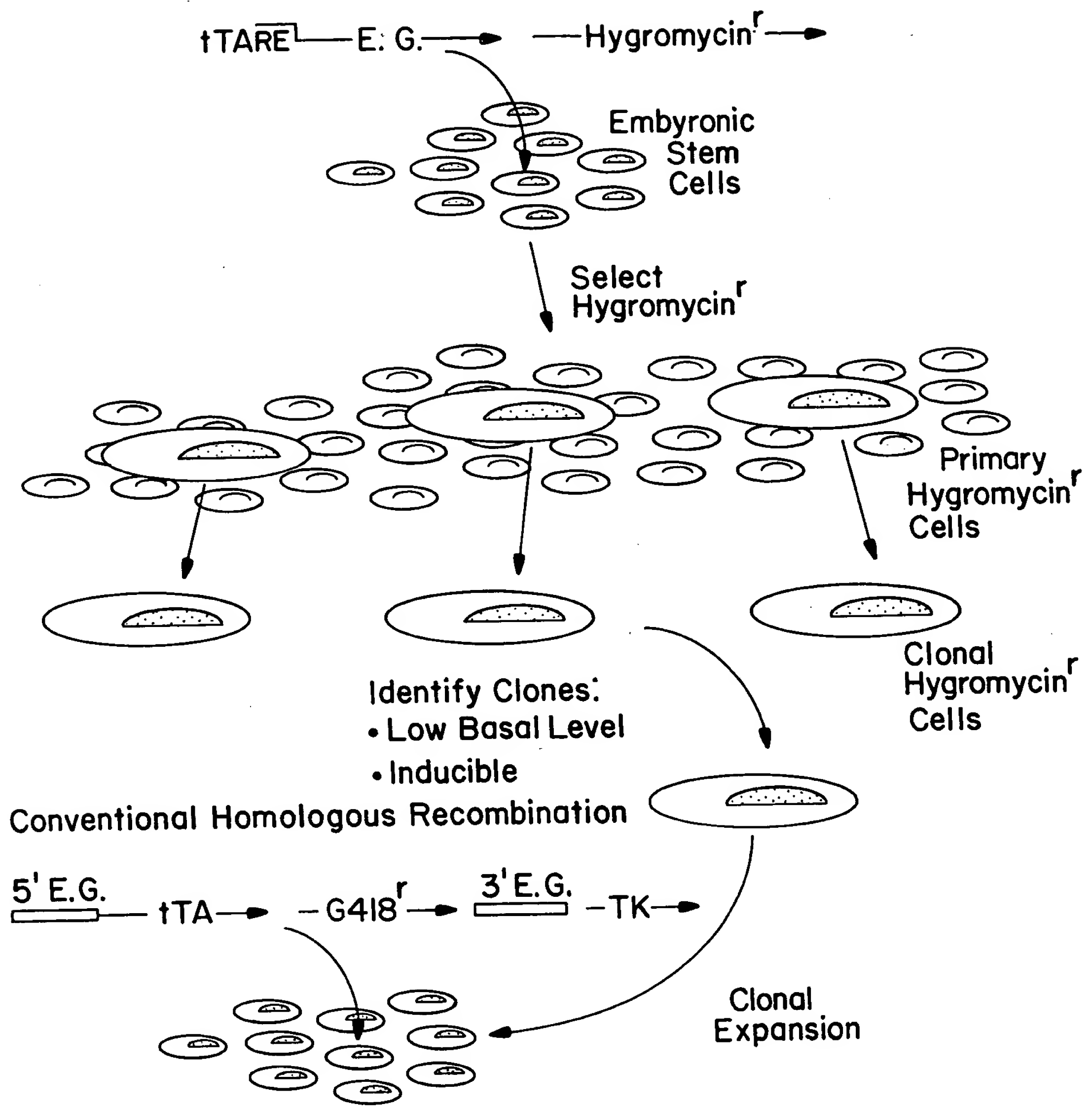


FIG. 12



SECRET

FIG. 13A

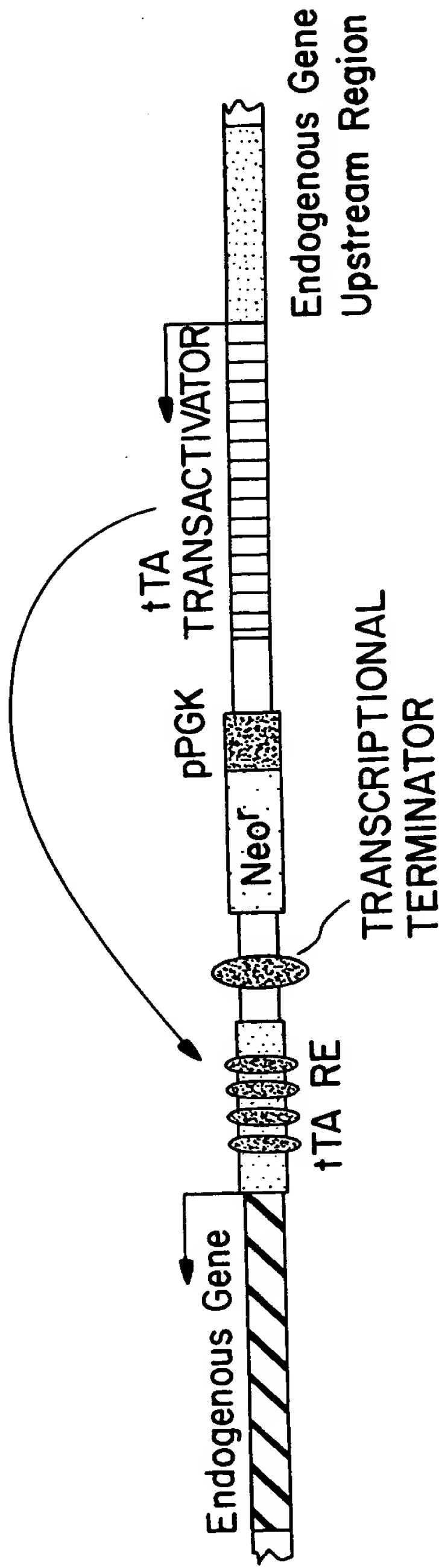
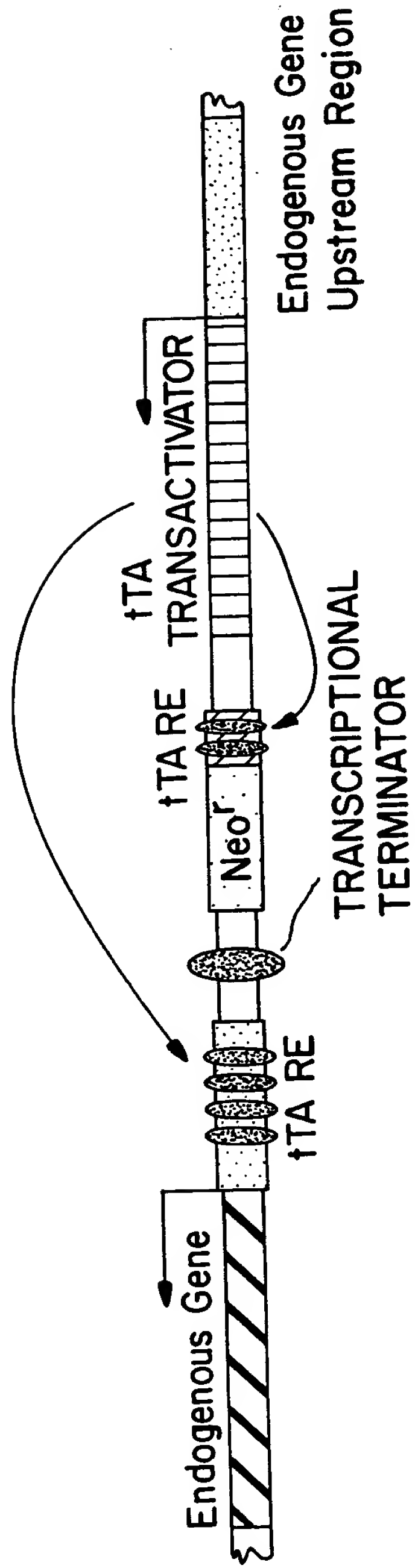
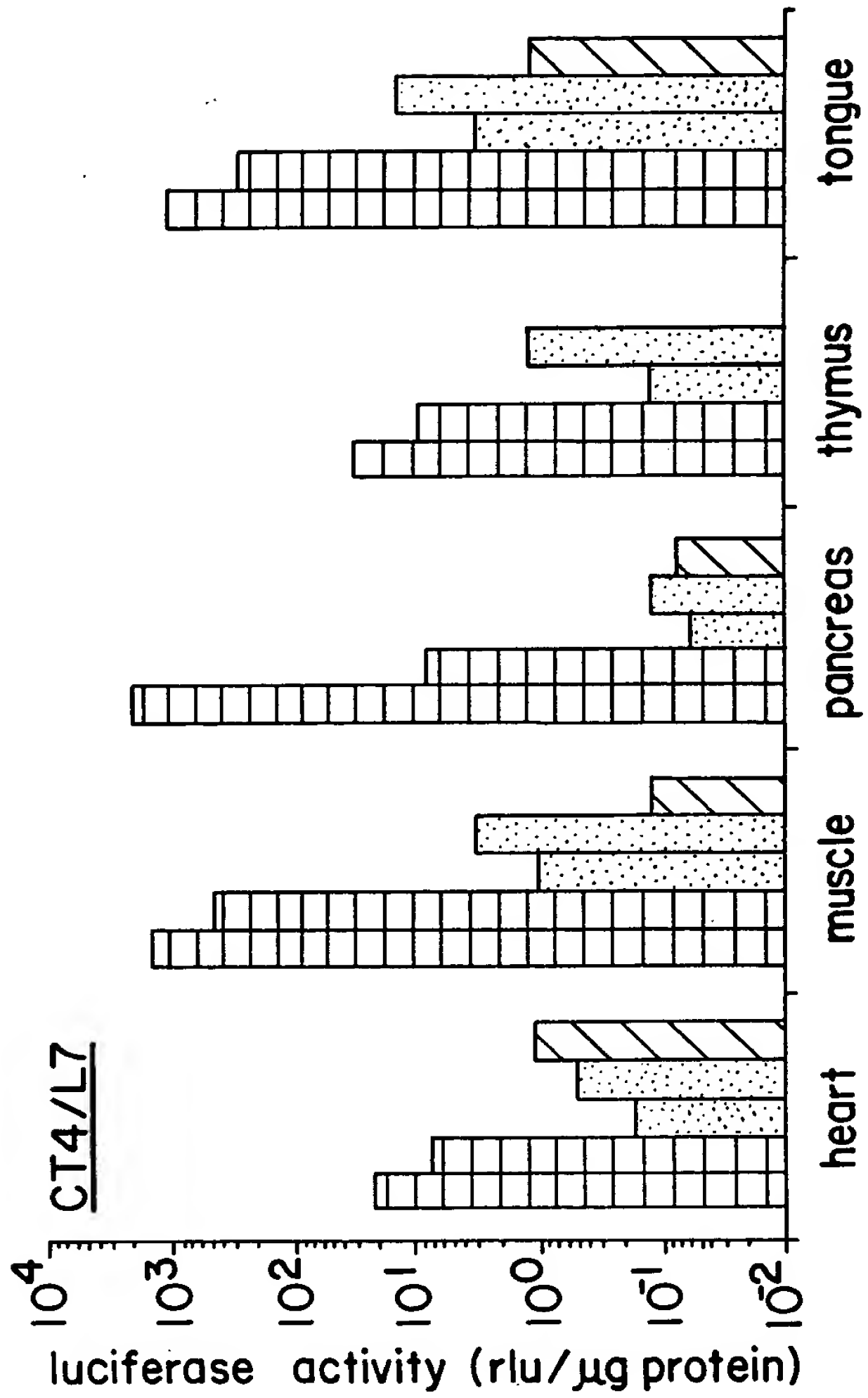


FIG. 13B



650860-42373260

FIG.14



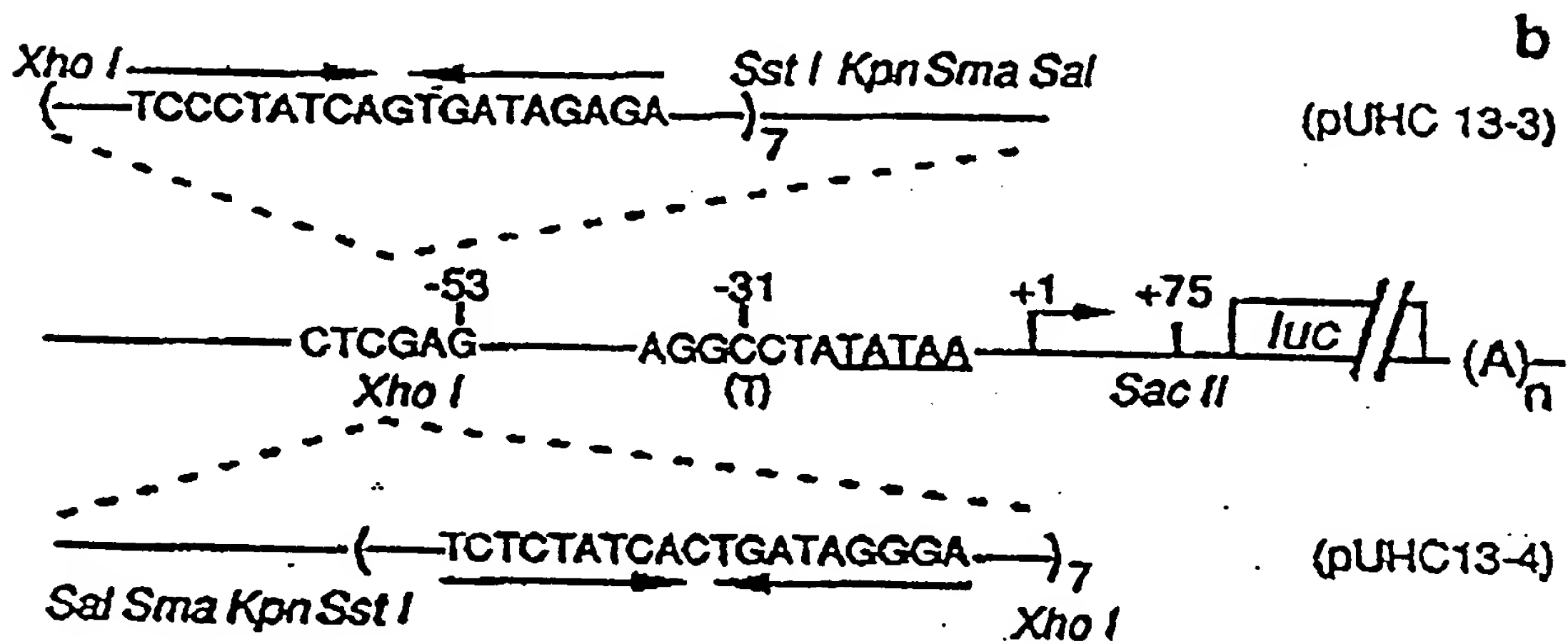
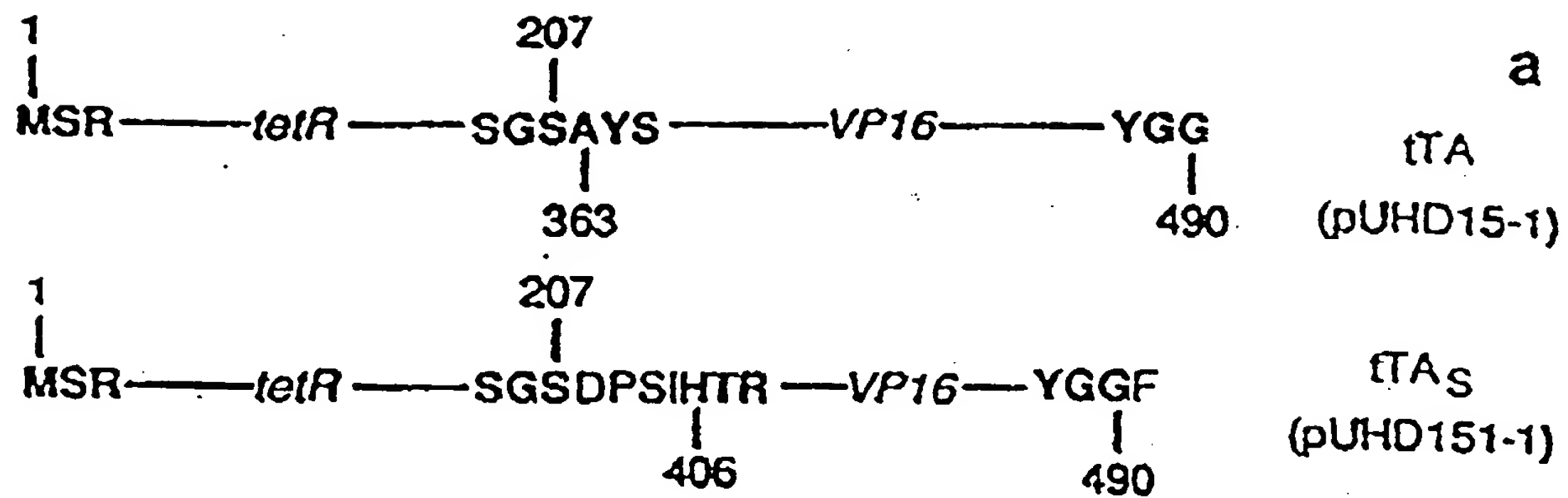


Fig. 1

a

	C		N	
	-	+	-	+
kDa				
66				
45				
36				
29				
24				

b

1	2	3	4	5

Fig. 2

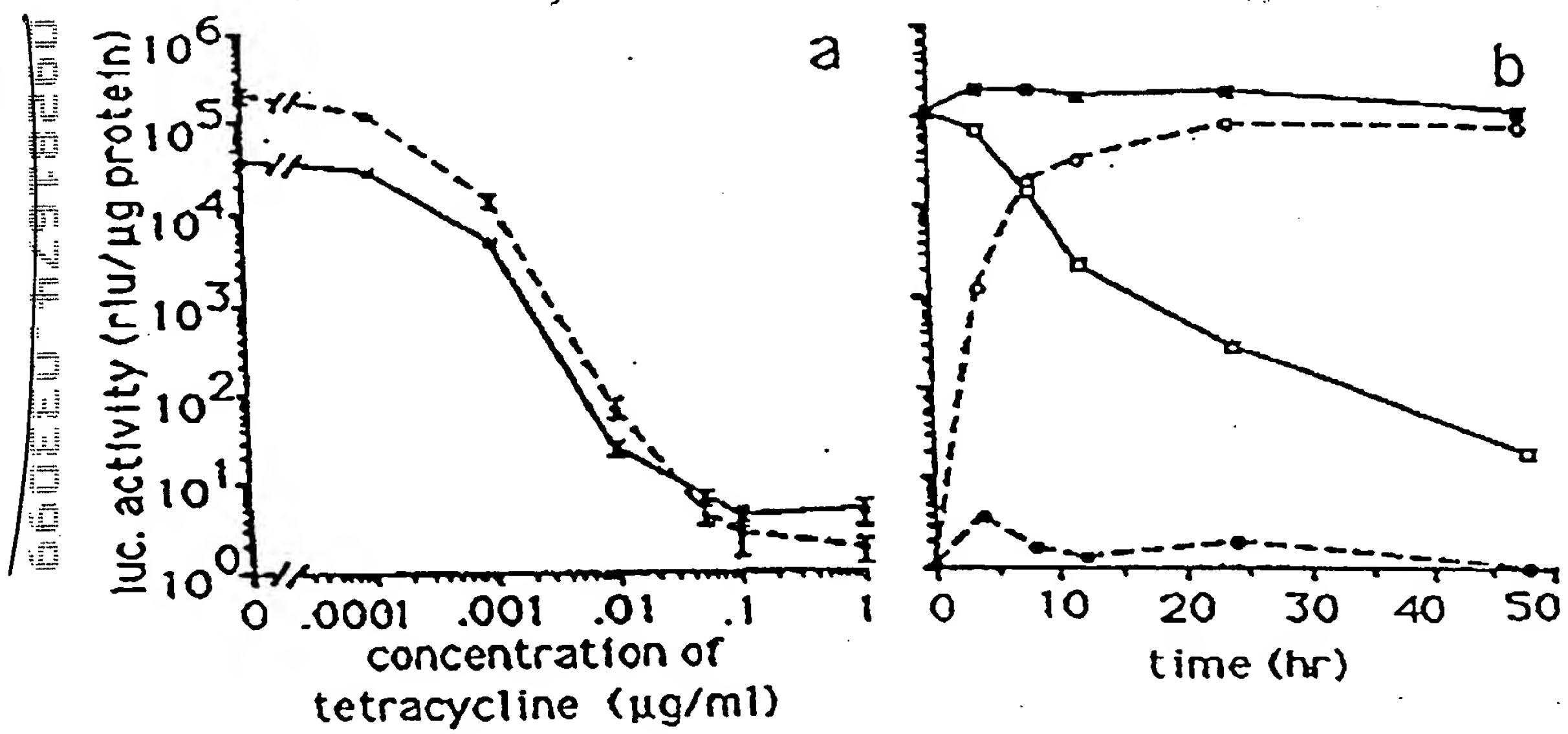


Fig. 3

1/1	ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AOC OCA TTA GAG CTC CTT AAT GAG GTC	31/11	
Met ser arg leu asp lys ser lys val ile	asn ser ala leu glu leu leu asn glu val	91/31	
51/21	GGA ATC GAA GGT TTA ACA ACC GGT AAA CTC GCC CAG AAG CTA GGT GTA GAG CAC CCT ACA		
gly ile glu gly leu thr thr arg lys leu	ala gln lys leu gly val glu gln pro thr	151/51	
121/41	TTG TAT TCG CAT GTA AAA AAT AAG GGG GCT TTG CTC GAC CCC TTA CCC ATT GAG ATG TTA		
leu tyr trp his val lys asn lys arg ala	leu leu asp ala leu ala ile glu met leu	211/71	
181/61	CAT AGG CAC CAT ACT CAG TTT TGG OCT TTA GAA GGG GAA AGC TGG CAA CAT TTT TTA CCT		
asp arg his his thr his phe cys pro leu	glu gly glu ser trp gln asp phe leu arg	271/91	
241/81	AAT AAG CCT AAA AGT TTT ACA TGT OCT TTA CTA AGT CAT OGC GAT GGA GCA AAA GTA CAT		
asn lys ala lys ser phe arg cys ala leu	leu ser his arg asp gly ala lys val his	331/111	
301/101	TTA GGT ACA GGG CCT ACA GAA AAA CAG TAT GAA ACT CTC GAA AAT CAA TTA GGC TTT TTA		
leu gly thr arg pro thr glu lys gln tyr	glu thr leu glu asn gln leu ala phe leu	391/131	
361/121	TGC CAA CAA GGT TTT TCA CTA GAG AAT GCA TTA TAT GCA CTC AGC OCT OTG GGG CAT TTT		
cys gln gln gly phe ser leu glu asn ala	leu tyr ala leu ser ala val gly his phe	451/151	
421/141	ACT TTA GGT TGC GTA TTG GAA CAT CAA CAC CAT CAA GTC GGT AAA CAA CAA AGC CAA ACA		
thr leu gly cys val leu glu asp gln glu	his gln val ala lys glu glu arg glu thr	511/171	
481/161	OCT ACT ACT GAT AGT ATG CCG OCA TTA TTA CCA CAA OCT ATC GAA TTA TTT GAT CAC CAA		
pro thr thr asp ser met pro pro leu leu	arg gln ala ile glu leu phe asp his gln	571/191	
541/181	GGT GCA GAG OCA GGC TTC TTA TTC GGC CTT GAA TTG ATC ATA TGC GGA TTA GAA AAA CAA		
gly ala glu pro ala phe leu phe gly leu	glu leu ile ile cys gly leu glu lys gln	631/211	
601/201	CTT AAA TGT GAA ACT GCG TCC GCG TAC AGC GCG GCG GGT ACC AAA AAC AAT TAC GGG TGT		
leu lys cys glu ser gly ser ala tyr ser	arg ala arg thr lys asn asn tyr gly ser	691/231	
661/221	ACC ATC GAG GGC CTG CTC GAT CTC CCG GAC GAC GAC GGC CCC CAA GAG GCG GGG CTG GCG		
thr ile glu gly leu leu asp leu pro asp	asp asp ala pro glu glu ala gly leu ala	751/251	
721/241	GCT CCG GCG CTG TCC TTT CTC CCG GCG GGA CAC AGC GCG ACA CTG TCG AGC GGC CCC CCG		
ala pro arg leu ser phe leu pro ala gly	his thr arg arg leu ser thr ala pro pro	811/271	
781/261	ACC GAT GTC AGC CTG GGG GAC GAG CTC CAC TTA GAC GGC GAG GAC GTG GCG ATC CCG CAT		
thr asp val ser leu gly asp glu leu his	leu asp gly glu asp val ala met ala his	871/291	
841/281	GCG GAC GCG CTA GAC GAT TTC GAT CTG GAC ATC TTG GCG GAC GCG GAT TCC CCG GGT CCG		
ala asp ala leu asp asp phe asp leu asp	met leu gly asp gly asp ser pro gly pro	931/311	
901/301	GGA TTT AOC CCG CAC GAC TCC GCG CCG TAC GCG GCT CTG GAT ATG GCG GAC TTC CAC TTT		
gly phe thr pro his asp ser ala pro tyr	gly ala leu asp met ala asp phe glu phe	991/331	
961/321	GAG CAG ATG TTT ACC GAT CCG CTT GGA ATT CAC GAG TAC GGT GCG TAG		
glu gln met phe thr asp pro leu gly ile	asp glu tyr gly gly AMB		

Fig. 4

1/1	ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG CTT AAT CAG CTC	31/11
Met ser arg leu asp lys ser lys val ile	asn ser ala leu glu leu leu asn glu val	
61/21	GGA ATC CAA GGT TTA ACA ACC CGT AAA CTC CCC CAG AAC CTA OCT GTA GAG CAG CCT ACA	91/31
gly ile glu gly leu thr thr arg lys leu	ala gln lys leu gly val glu gln pro thr	
121/41	TTG TAT TGC CAT GTA AAA AAT AAG CCG OCT TTC CTC CAC GGC TTA GGC ATT CAG ATG TTA	151/51
leu tyr trp his val lys asn lys arg ala	leu leu asp ala leu ala ile glu met leu	
181/61	GAT AGG CAC CAT ACT CAC TTT TGC CCT TTA GAA GGG GAA AOC TGG CAA GAT TTT TTA OCT	211/71
asp arg his his thr his phe cys pro leu	glu gly glu ser trp gln asp phe leu arg	
241/81	AAT AAC GGT AAA AGT TTT ACA TGT CCT TTA CTA AGT CAT GGC GAT GCA GCA AAA GTA CAT	271/91
asn asn ala lys ser phe arg cys ala leu	leu ser his arg asp gly ala lys val his	
301/101	TTA GGT ACA CCG OCT ACA GAA AAA CAG TAT CAA ACT CTC GAA AAT CAA TTA GGC TTT TTA	331/111
leu gly thr arg pro thr glu lys gln tyr	glu thr leu glu asn gln leu ala phe leu	
361/121	TGC CAA CAA GGT TTT TCA CTA GAG AAT GCA TTA TAT GCA CTC AGC OCT GTC GGC CAT TTT	391/131
cys gln gln gly phe ser leu glu asn ala	leu tyr ala leu ser ala val gly his phe	
421/141	ACT TTA GGT TGC GTA TTC GAA CAT CAA GAG CAT CAA GTC GGT AAA GAA GAA AGG CAA ACA	451/151
thr leu gly cys val leu glu asp gln glu	his gln val ala lys glu glu arg glu thr	
481/161	CCT ACT ACT CAT AGT ATG CCG CCA TTA TTA GGA GAA OCT ATC GAA TTA TTT CAT CAC CAA	511/171
pro thr thr asp ser met pro pro leu leu	arg gln ala ile glu leu phe asp his gln	
541/181	GCT GCA GAG CCA GGC TTC TCA TTC GGC CTT GAA TTC ATC ATA TGC GGA TTA GAA AAA CAA	571/191
gly ala glu pro ala phe leu phe gly leu	glu leu ile ile cys gly leu glu lys gln	
601/201	CTT AAA TGT CAA AGT GGG TCT GAT CCA TCG ATA CAC ACG GGC AGA CTG TCG ACG GGC CCC	631/211
leu lys cys glu ser gly ser asp pro ser	ile his thr arg arg leu ser thr ala pro	
661/221	CCG AOC GAT CTC AOC CTG GGG GAC GAG CTC CAC TTA GAC GGC GAG GAC GTC GCG ATG GCG	691/231
pro thr asp val ser leu gly asp glu leu	his leu asp gly glu asp val ala met ala	
721/241	CAT GCG GAC GCG CTA GAC GAT TTC GAT CTC CAC ATG TTG GCG CAC GGC CAT TCC CCG OCT	751/251
his ala asp ala leu asp asp phe asp leu	asp met leu gly asp gly asp ser pro gly	
781/261	CCG GGA TTT AOC CCG CAC GAC TCC GCG CTT TAC GGC OCT CTG GAT ATG GCG GAC TTC CAG	811/271
pro gly phe thr pro his asp ser ala pro	tyr gly ala leu asp met ala asp phe glu	
841/281	TTT GAG CAG ATG TTT AOC GAT GCG CTT GGA ATT GAC GAG TAC OCT GCG TTC TAG	871/291
phe glu gln met phe thr asp ala leu gly	ile asp glu tyr gly gly phe AMB	

Fig. 5

GAATTCCTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTC
CCTATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGT
GAAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCC
TATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGA
AAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGCTCGGTACCCGGGT
CGAGTAGGCGTGTACGGTGGGAGGCCATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGC
CTGGAGACGCCATCCACGCTGTTTGGACCTCCATAGAAGACACCGGGACCGATOCAGCCTCCGC
GG

Fig. 6

GAATTCCTCGACCCGGGTACCGAGCTCGACTTTCACCTTTCTCTATCACTGATAGGGAGTGGTA
AACTCGACTTTCACCTTTCTCTATCACTGATAGGGAGTGGTAAACTCGACTTTCACCTTTCTCT
ATCACTGATAGGGAGTGGTAAACTCGACTTTCACCTTTCTCTATCACTGATAGGGAGTGGTAAA
CTCGACTTTCACCTTTCTCTATCACTGATAGGGAGTGGTAAACTCGACTTTCACCTTTCTCTAT
CACTGATAGGGAGTGGTAAACTCGACTTTCACCTTTCTCTATCACTGATAGGGAGTGGTAAACT
CGAGTAGGCGTGTAAGGTGGGAGGOCATATAAGCAGAGCTCGTTAGTGAACCGTCAGATCGC
CTGGAGACGCCATOCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGC
GG

Fig. 7

GAGCTCGACTTTCACITTTCTCTATCACTGATAGGGAGTGGTAAACTCGACTTTCACITTTCTC
TATCACTGATAGGGAGTGGTAAACTCGACTTTCACITTTCTCTATCACTGATAGGGAGTGGTAA
ACTCGACTTTCACITTTCTCTATCACTGATAGGGAGTGGTAAACTCGACTTTCACITTTCTCTA
TCACTGATAGGGAGTGGTAAACTCGACTTTCACITTTCTCTATCACTGATAGGGAGTGGTAAAC
TCGACTTTCACITTTCTCTATCACTGATAGGGAGTGGTAAACTCGAGATCCGGGGAATTCGAAC
ACGCAGATGCAGTCGGGGCGGCGGGTCGAGGTCCACTTCGCATATTAAGGTGACGGGTGTGG
CCTCGAACACCGAG

Fig. 8

Fig. 9A

CTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATC
AGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGT
CGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATCAG
TGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCG
AGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGCTGGGTACCGGGTCGAGTA
GGCGTGTCGGGTGGGAGGCTATATAAGCAGAGCTCGTTTGTGTAACCGTCAGATCGCCTGGAG
ACGCCATCCACGCTGTTTTGACCTCCATAGAGACACCGGGACCGATCCAGCCTCCGCGCCCCC
GAATTGAGCTCGGTACCGGGCCCCCCCCCTCGAGGTCCGACGGTATCGATAAGCTTGATATCGAAT
TCCAGGAGGTGGAGATCCGCGGGTCCAGCCAAACCCACACCCATTTTCTCCTCCCTCTGCCCC
TATATCCCGGCCACCCCCCTCCTCCTAGCCCTTTCCCTCCTCCCGAGAGACGGGGGAGGAGAAAAG
GGGAGTTCAGGTTCGACATGACTGAGCTGAAGGCCAAAGGAACCTCGGGCTCCCCACGTGGCGGGC
GGCGCGCCCTCCCCACCGAGGTTCGGATCCAGCTCCTGGGTCCCGCGGACCCCTGGCCCCCTTCC
AGGGGAGCCAGACCTCAGAGGCTCGTCTGTAGTCTCGGCCATCCCATCTCCTTGGACGGGT
GCTCTTCCCCCGGCCCTGTTCAGGGGCAGAACCCCCCAGACGGGAAGACGCAGGAOCCACCGTCG
TTGTTCAGACGTGGAGGGGCGCATTTCTGAGTCCGAAGCCCCCGAGGGGGCAGGAGACAGCAGCT
CGAGACCTCCAGAAAAGGACAGCGGCTGCTGGACAGTGTCTCTGACACGCTCCTGGCGCCCTC
GGGTCCCGGGCAGAGCCACGCCAGCCCTGCCACCTGCGAGGCCATCAGCCCGTGGTGCCCTGTTT
GGCCCCGACCTTCCCGAAGACCCCCGGGCTGCCCCCGCTACCAAGGGGTGTGTGGCCCCGCTCA
TGAGCCGACCCGAGGACAAGGCAGGCGACAGCTCTGGGACGGCAGCGGCCACAAAGGTGCTGCC
CAGGGGACTGTACCATCCAGGCAGCTGCTGCTCCTCCTCTGGGAGCCCTCACTGGCCCGCA
GTGAAGCCATCCCGCAGCCCGCTGCGGTGCAGGTAGACGAGGAGGACAGCTCCGAATCCGAGG
GCACCGTGGGCCCCGCTCCTGAAGGGCCAACCTCGGGCACTGGGAGGCACGGCGGCGGGAGGAGG
AGCTGCCCCCGTGGCGTCTGGAGGGCCCGCAGGAGGGGTGCGCCCTTGTCCCCAAGGAAGATTCT
CGCTTCTCGGCGCCCAAGGTCTCCTTGGCGGAGCAGGACGCGCCGGTGGCGCCTGGGGGCTCCC
CGCTGGCCACCTCGGTGGTGGATTTCATCCACGTGCCCATCCTGCTCTCAACCCAGCTTTCT
GGCCACCCGACACAGGCAGCTGCTGGAGGGGGAGAGCTACGAAGCGGGGGCGCGGGCCGCGCAGC
CCCTTCGTCCCGCAGCGGGGCTCCCCCTCTGCTCCTCCACCCCTGTGGCGGGCGGCGACTTCC
CCGACTGCACCTACCCGCCCCGACGCGGAGGCCAAAGATGACGCGTTCCCCCTCTACGGCGACTT
CCAGCCGCCCCGCCCCCAAGATAAAGGAGGAGGAAGAAGCCGCGAGGCGCGCGCGCTCCCCG
CGTACGTACCTGGTGGCTGGTGCAAACCCCGCGCGCTTCCCGGACTTCCAGCTGGCAGCGCGC
CGCCACCCCTCGCTGCCGCTCGAGTGCCCTCGTCCAGAACCGGGGAAGCGCGGTGGCGGCTC

[illegible]

Fig. 9C

CTCTOCTGTTTCOGACCOCTGCCGCTTACCGGATACCTGTCCGCCCTTTCCTCCCTTTOGGGAAGCGTG
GCGCTTTCCTCAATGCTCAGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCCCTCCAAGCTGG
GCTGTGTGCACGAACCCCCCGTTTACGCCCGACCGCTGCGCCTTATCCGGTAACCTATCGTCTTGA
GTCCAACCCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA
GCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAA
GGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCCGAAAAGAGTTGGTAGCTC
TTGATCCGGCAACAAACCAACCGCTGGTAGCGGTGGTTTTTTTTTGTGTTGCAAGCAGCAGATTACG
CGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACCGCTCAGTGGA
ACGAAAACCTCACGTTAAGGCATTTTGGTTCATGAGATTATCAAAAAGGATCTTCAOCTAGATCCT
TTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATAATGAGTAAACTTGGTCTGACAGT
TACCAATGCTTAAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCAATCCATAGTTG
CCTGACTCCCCGTCGTGTAGATAACTACGATAAGGGAGGGGCTTACCATCTGGCCCCAGTGCTGC
AATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGA
AGGGCCGAGCGCAGAAAGTGGTCCCTGCAACTTTATCCGCCCTCCATCCAGTCTATTAATTGTTGCC
GGGAAGCTAGAGTAAGTAGTTCCGCCAGTTAATAGTTTGGCGCAACGTTGTTGCCATTGCTACAGG
CATCGTGGTGTACCGCTCGTCTGTTTGGTATGGCTTCATTTCAGCTCCGGTTCCCAACGATCAAGG
CGAGTTACATGATCCOCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCCGGTCTCCGATCGTTG
TCAGAAGTAAGTTGGCCGCGAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTAC
TGTCTATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAOCCAAGTCATTCTGAGAA
TAGTGTATGCGGCGACCGAGTTGCTCTTGGCCGGCGTCAATACGGGATAATAOCCGCGCCACATA
GCAGAACTTTAAAAGTGCTCATCATTTGGAAAAGGTTCTTCCGGGGGGAATACTCTCAAGGATCTT
ACCGCTGTTGAGATCCAGTTTCGATGTAAOCCACTCGTGCACCCAACTGATCTTCAGCATCTTTT
ACTTTCACCAGOGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAA
GGGCGACACGGAAATGTTGAATACTCATACTCTTCCCTTTTCAATATTATTGAAGCATTATCA
GGGTTATTGTCTCATGAGCGGATACATATTGAATGTATTTAGAAAAATAAACAATAGGGGTT
CCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTTATTATCATGACATTAA
CCTATAAAAATAGGCGTATCACGAGGCGCCTTTCGTC

Fig. 10A

CTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATC
 AGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGT
 CGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATCAG
 TGATAGAGAAAAGTGAAAGTCGAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCG
 AGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTCGAGCTCGGTACCCGGGTCGAGTA
 GCGGTGTACGGTGGGAGGCCTATATAAGCAGAGCTCGTTTGTAGTGAACCGTCAGATCGCCTGGAG
 ACGCCATCCAGCTGTMTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGGGGCCCC
 GAATTCGGGCCACGACCATGACCATGACCCCTCCACACCAAGCATCTGGGATGGCCCTACTGCA
 TCAGATCCAAGGGAACGAGCTGGAGCCCTGAACCGTCGCGAGCTCAAGATCCCCCTGGAGGGG
 CCCCCTGGGCGAGGTGTACCTGGACAGCAGCAAGCCCGCCGTGTACAACTACCCCGAGGGGCGCG
 CCTACGAGTTCAACGCCGCGCGGCCGCCAAGCGCGCAGGTCTACGGTCAGACCGGCCTCCCTTA
 CGGCCCGGGTCTGAGGCTGCGGGGTTCGGCTCCAACGGCCTGGGGGGTTTCCCCCCTCAAC
 AGCGTGTCTCCGAGCCCGCTGATGCTACTGCAACCCGCGCGCCAGCTGTCCGCTTTCTGTCAGC
 CCCACGGCCAGCAGGTGCCCTACTACCTGGAGAAACAGCCAGCGGCTACACGGTGGCGGAGGC
 CGGCCCGCCGGCATTTCTACAGGCCAAATTCAGATAATCGACGCCAGGGTGGCAGAGAAAGATTG
 GCCAGTACCAATGACAAGGGAAGTATGGCTATGGAATCTGCCAAGGAGACTCGCTACTGTGCAG
 TGTGCAATGACTATGCTTCAGGCTACCATTTATGGAGTCTGGTCTGTGAGGGCTGCAAGGCCTT
 CTTCAAGAGAAGTATTCAGGACATAACGACTATATGTGTCCAGCCACCAACCAGTGCACCATT
 GATAAABACAGGAGGAAGAGCTGCCAGGCCTGCCGGCTCCGCAATGCTACGAAGTGGGAATGA
 TGAAAGGTGGGATACGAAAAGACCGAAGAGGAGGGAGAATGTTGAAACACAAGCGCCAGAGAGA
 TGATGGGGAGGGCAGGGGTGAAGTGGGGTCTGCTGGAGACATGAGAGCTGCCAACCTTTGGCCA
 AGCCCGCTCATGATCAAACGCTCTAAGAAGAACAGCCTGGCCTTGTCCCTGACGCGCCGACCAGA
 TGGTCATGGCCTTGTGGATGCTGAGCCCCCATACTCTATTCCGAGTATGATCCTACCAGACC
 CTTCACTGAAGCTTCGATGATGGGCTTACTGACCAACCTGGCAGACAGGGAGCTGGTTTACATG
 ATCAACTGGGCGAAGAGGGTGGCAGGCTTTGTGGATTTGACCCCTCCATGATCAGGTCCACCTTC
 TAGAATGTGCCTGGCTAGAGATCCTGATGATTTGGTCTCGTCTGGCGCTCCATGGAGCACCCAGT
 GAAGCTACTGTTTGTCTCCTAACTTGCTCTTGGACAGGAACAGGGGAAATGTGTAGAGGGCATG
 GTGGAGATCTTCGACATGCTGCTGGCTACATCATCTCGGTTCGCGCATGATGAATCTGCAGGGAG
 AGGAGTTTGTGTGCCCTCAAATCTATTATTTTGTCTTAATTCTGGAGTGTACACATTTCTGTCCAG
 CACCTTGAAGTCTCTGGAAGAGAAGGACCATATCCACCGAGTCTCTGGACAAGATCACAGACACT
 TTGATCCACCTGATGGCCAAGGCAGGCTTGACCTGCAGCAGCAGCAGCAGCGGCTGGCCCCAGC
 TCCTCCTCATCCTCTCCACATCAGGCACATCAGTAACAAAGGCATGGAGCATCTGTACAGCAT
 GAAGTGCAAGAACGTGGTGGCCCTCTATGACCTGCTGCTGGAGATGCTGGACGCCACCGCCTA
 CATGCGGCCACTAGCCGTGGAGGGGCATCCGTGGAGGAGACGGACCAAGCCACTTGGCCACTG
 CGGGCTCTACTTCATCGCATTCCTTGCAAAAGTATTACATCACGGGGGAGGCGAGGGGTTTCCC
 TGCCACAGTCTGAGAGCTCCCTGGCGGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGGATC
 CAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATG
 CTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAAACCTTATAAGCTGCAATAACAA
 GTTAACAACAACAATTGCATTTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTMTT
 AAAGCAAGTAAAACCTCTACAAATGTGGTATGGCTGATTATGATCCTGCAAGCCTCGTCTCTG

Fig. 10B

GCCGGACACGCTATCTGTGCAAGGTCCCCGACGCGCGCTCCATGAGCAGAGCGCCCGCCGCC
GAGGCAAGACTCGGGCGGCGCCCTGCCCGTCCCACCAGGTCAACAGGCGGTAAACGGCCCTCTTC
ATCGGGAATGCGCGCGAOCCTTCAGCATCGCCGGCATGTCCCCCTGGCGGACGGGAAGTATCAGCT
CGACCAAGCTTGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAATCACTGGAT
ATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGGAGGCATTTTCAGTCAGTTGC
TCAATGTACCTATAACCAGACCGTTTCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGC
CCTTTGCGTATTGGGCGCTCTTCCGCTTCCCTCGCTCACTGACTCGCTGCGCTCGGTGCTTGGC

TGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACAGAATCAGGGGATAA
CGCAGGAAGAACATGTGAGCAAAAGGCCACCAAAAGGCCAGGAACCGTAAAAAGGCCCGCGTTG
CTGGCGTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGA
GGTGGGAAACCCGACAGGACTATAAGATAACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCG
CTCTCCTGTTCGACCCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG
CGCTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCGCTCCAAGCTGG
GCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCCGCTTATCCGGTAACATATCGTCTTGA
GTCCAACCCCGGTAAAGACAGGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA
GCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTAAGGCTACACTAGAA
GGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTC
TTGATCCCGCAAACAAACCACCGCTGGTAGCGGTGGTTTFTTTGTGTTGCAAGCAGCAGATTACG
CGCAGAAAAAAGGATCTCAAGAAGATCCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGA
ACGAAAACTCACGTTAAGGGATTMTGGTCAATGAGATTATCAAAAGGATCTTCACCTAGATCCT
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CCTGATCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCOCCAGTGCTGCA
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GGGCCGAGCGCAGAAGTGGTCCGCAACTTTATCCGCTCCATCCAGTCTATTAAATTGTTGCCG
GGAAGCTAGAGTAAGTAGTTCCGCCAGTTAATAGTTTGGCGCAACGTTGTGTCATTGCTACAGGC
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GAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTGT
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GTCAATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAAT
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CAGAACTTTAAAGTGCTCATCATTTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTA
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CTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAG
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GGTTATTGTCTCATGAGCGGATACATATTGAATGTATTTAGAAAAATAAACAAATAGGGGTTTC
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Conditional Knock-Out Strategy 1

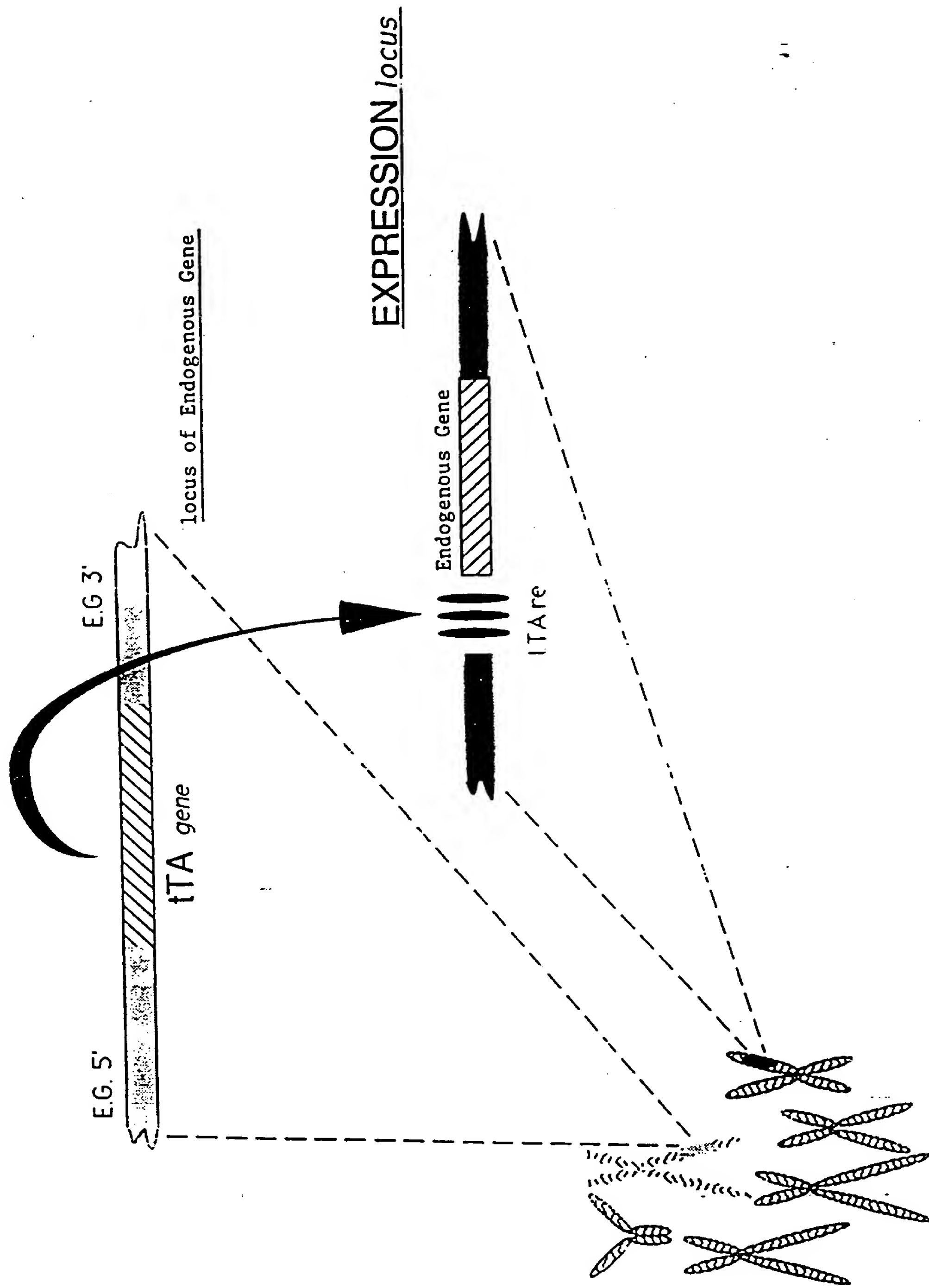
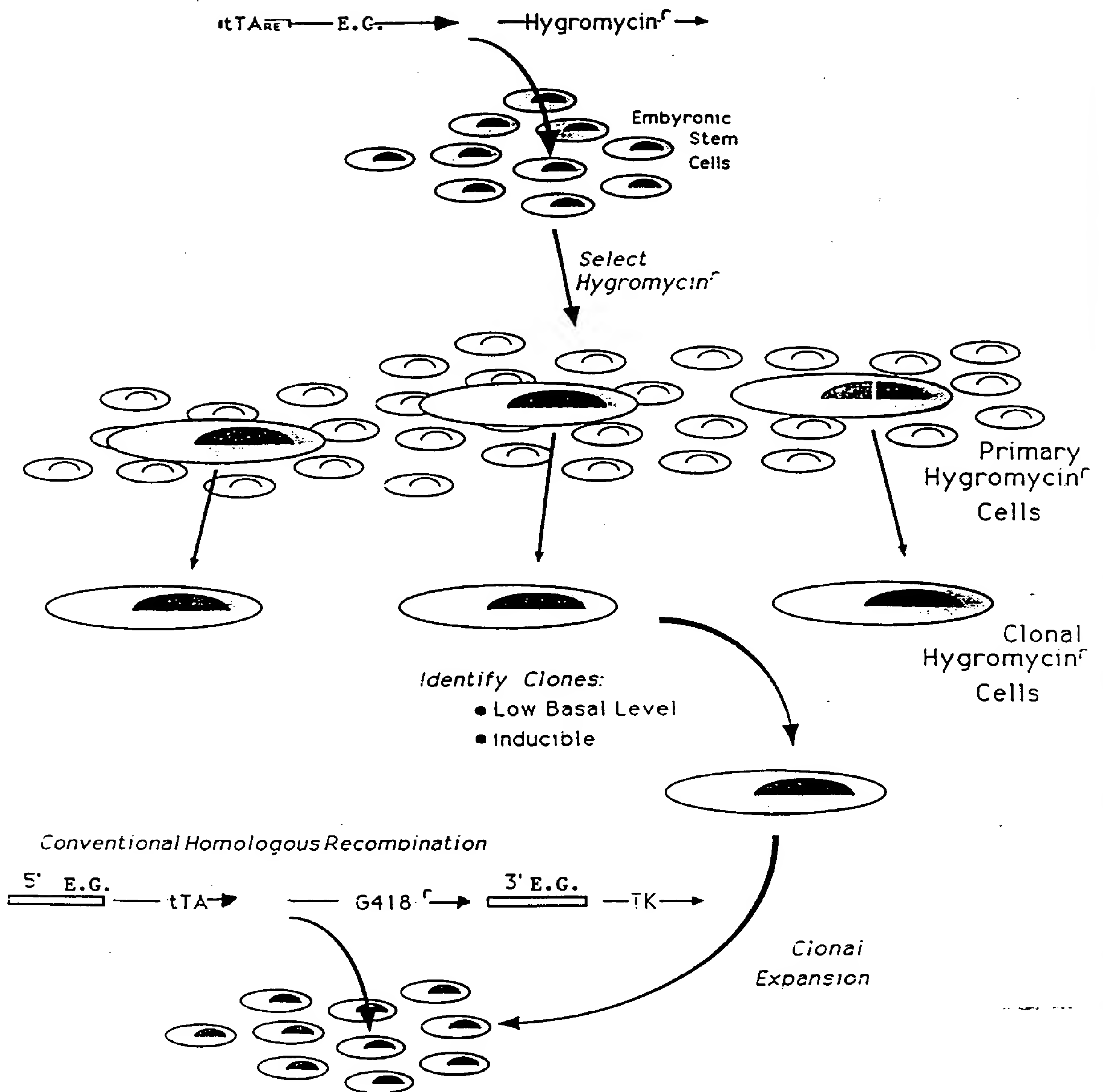


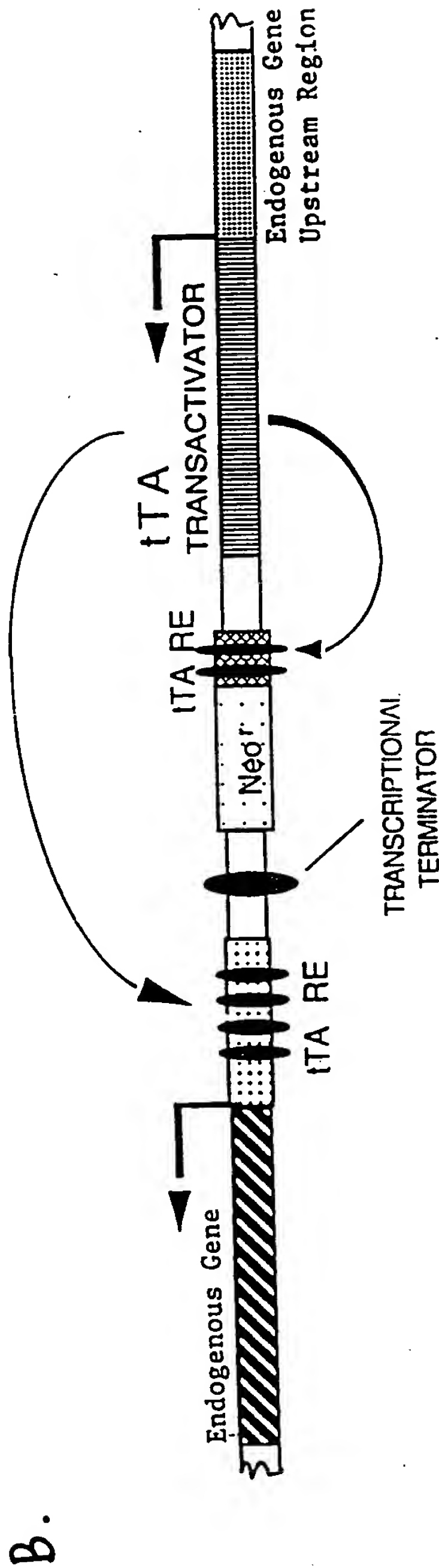
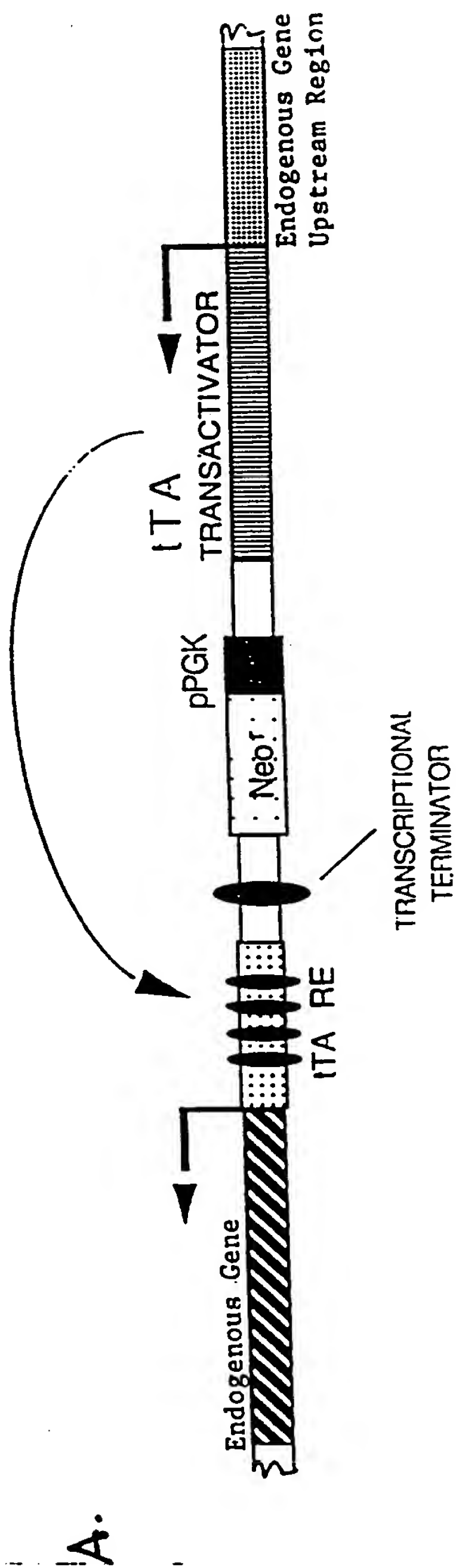
Fig. 12

Conditional Knock-Out Strategy 2



Identify clones with low basal activity of endogenous gene (near untransformed levels).
 Identify among these those which respond to tTA (by transient expression).
 Perform homologous recombination into endogenous locus.

Conditional Knock-Out Strategy 3



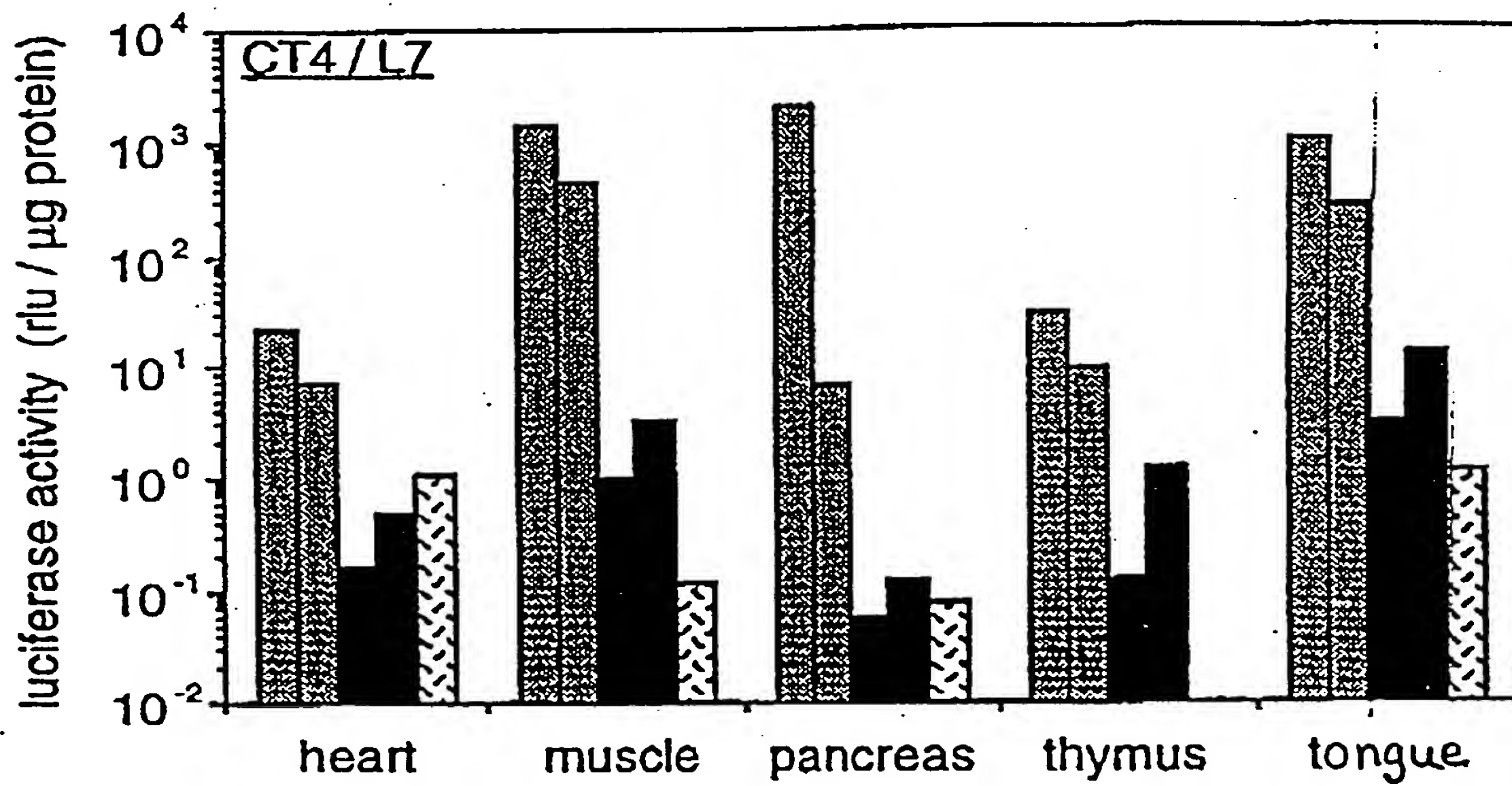


Figure 14